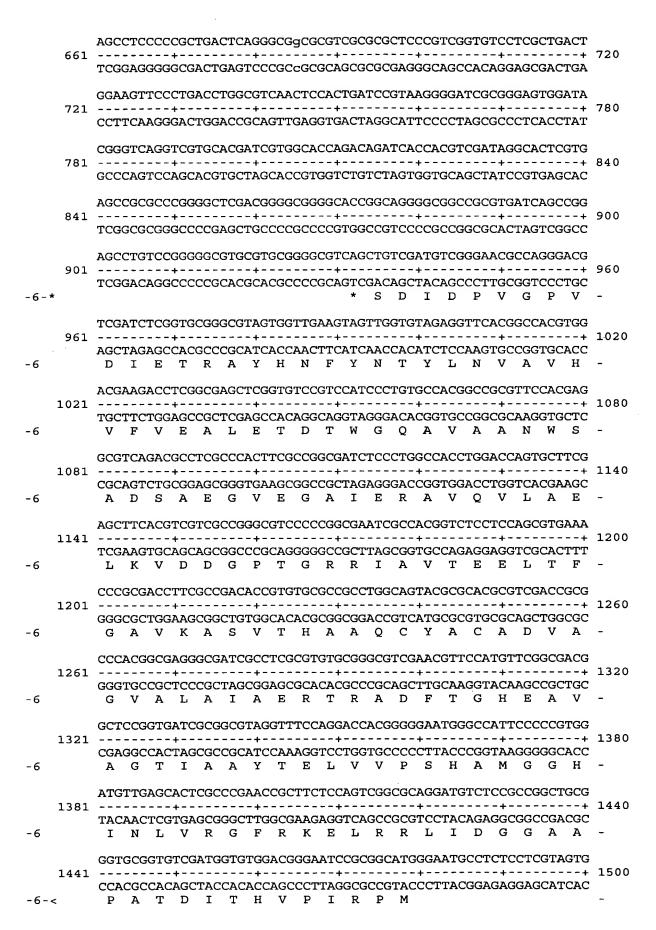
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SEQUENCE LISTING

SEQ ID No. 1. C-1027 gene cluster DNA sequence from 1 to 42,000, ORF-(-7) to ORF-26

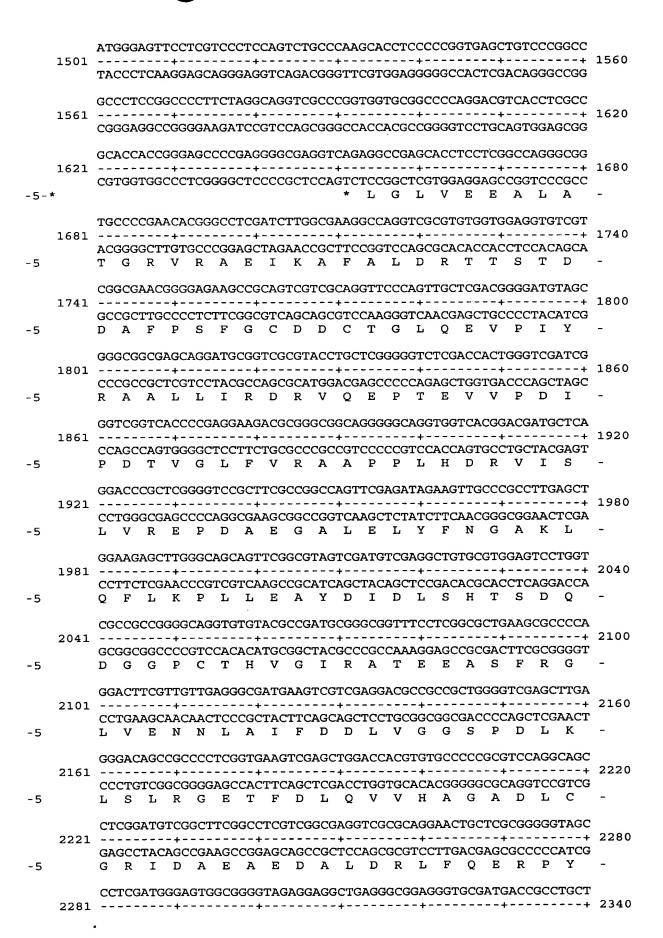
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-7-*	1	CAGCTGAGATCTCCTAGGGCCCACGCCTCATCCCCAATGCCTGCTTCCTCCCCACGGGCC * L I G P A S Y P N R V F S P H G	60 -
•	61	CGACGCCTGCGGCGAAGGGCGGTTCCTTGAGTTCGAGGCCGGTGGCGAGGACGACGTGGT	120
-7	91	GCTGCGGACGCCGCTTCCCGCCAAGGAACTCAAGCTCCGGCCACCGCTCCTGCTGCACCA A V G A A F P P E K L E L G T A L V V H	-
•	121	CCGCGTCGAGGATCTGCGTGTCGGGGAGGGGCCCAGGGCGCAGCCCCTCGGTCAGGTACG	180
-7		GGCGCAGCTCCTAGACGCACAGCCCCTCGCCGGGGTCCCGCGTCGGGGAGCCAGTCCATGC D A D L I Q T D P L P G P R L G E T L Y	-
-7	181	GGGTGAGGCCCTGACGGTCACCTCGAAGCAGCGGTCGTGGGACCGGGCGTCGAGCGCCT	240
		CCCACTCCGGGGACTGCCAGTGGAGCTTCGTCGCCAGCACCCTGGCCCGCAGCTCGCGGA PTLGRVTVEFCRDHSRADLA	-
	241	CCCCGTCCGCTTCCACAAGGACGACGCCGGGGCACAGGACTCCCGTGCGGCCTCGACCAGTC	300
-7		E G D A E V L V G P C S E R A A E V L	-
	301	GGGCGTCGAGGTAGTCCTGGAAGATGCGGCGGGGGGGGGG	360
-1		RADLYDQFIRRPAPGQETFK	-
	361	ACGAAGCCCAGCGCGGGCCAGTCGCGCCGGTCGGCCTCCTGGTTGGCCCAGTTGATGA	420
-7		W S A W R R P W D R R D A E Q N A W N I AGTCGAGCACGTCCTCGCGGAACACCGACATCCTGCCGGCCTGGATATTGAAGACGTGGT	-
	421	TCAGCTCGTGCAGGAGCGCCTTGTGGCTGTAGGACGCCCGGACCTATAACTTCTGCACCA	480
-7		F D L V D E R F V S M R G A Q I N F V H CCCAGGGGTTGCCGTCACGGTGATAGGCGACGCCGGCCGAGCGGTAGGCGCGCGC	-
7	481	GGGTCCCCAACGGCAGTGCCACTATCCGCTGCGGCCGCCTCGCCATCCGCCGCGCGCG	540
-7	541	CCAGGAGGACGACTTCCAGCGGTCTTCTCGCGAAATGAAGCAGGCGTATCGCGGTCGCCG	600
		GGTCCTCCTGCTGAAGGTCGCCAGAAGAGCGCTTTACTTCGTCCGCATAGCGCCAGCGGC E L L V V E L P R R A F H L L R I A T A	-
	601	TGCCTGCCAGGCCCGCCCCTACGACCAGCACCCTGGGGCGCGCACCCGTCATGCCCATGA	660
7 .	901	ACGGACGGTCCGGGGGATGCTGGTCGTGGGACCCCGGGCGTGGCAGTACGGGTACT	

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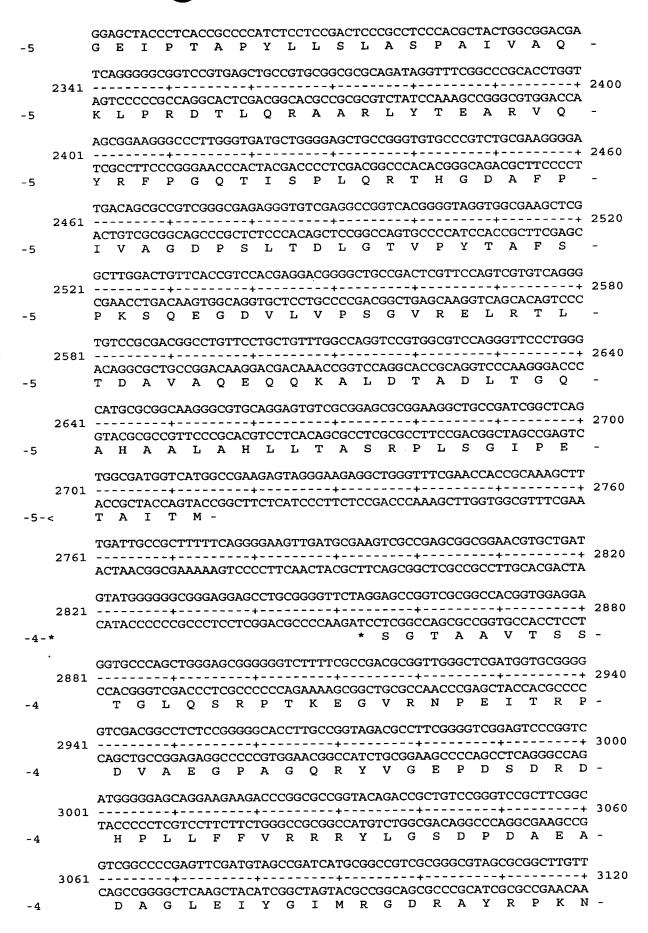
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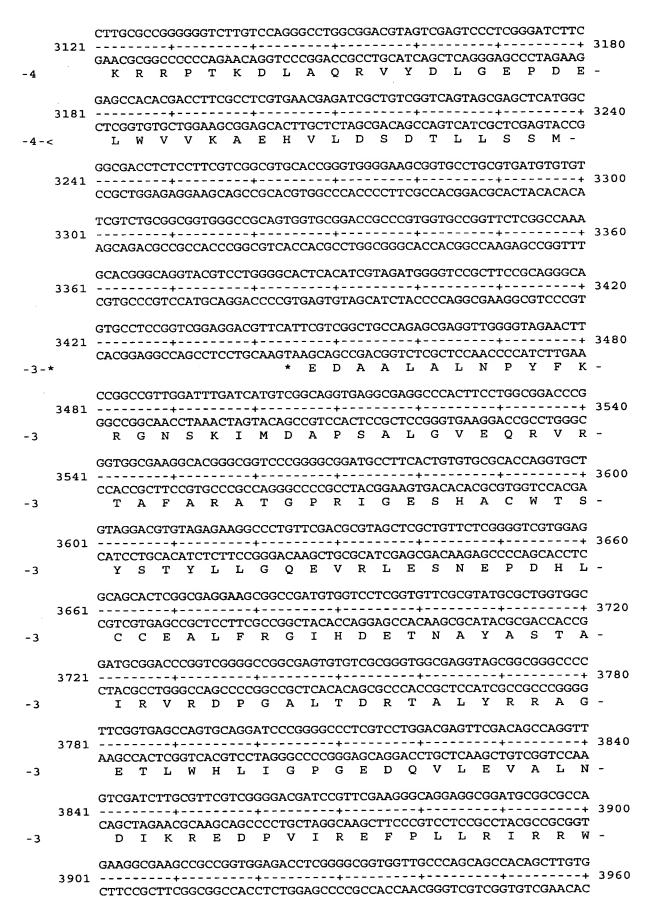
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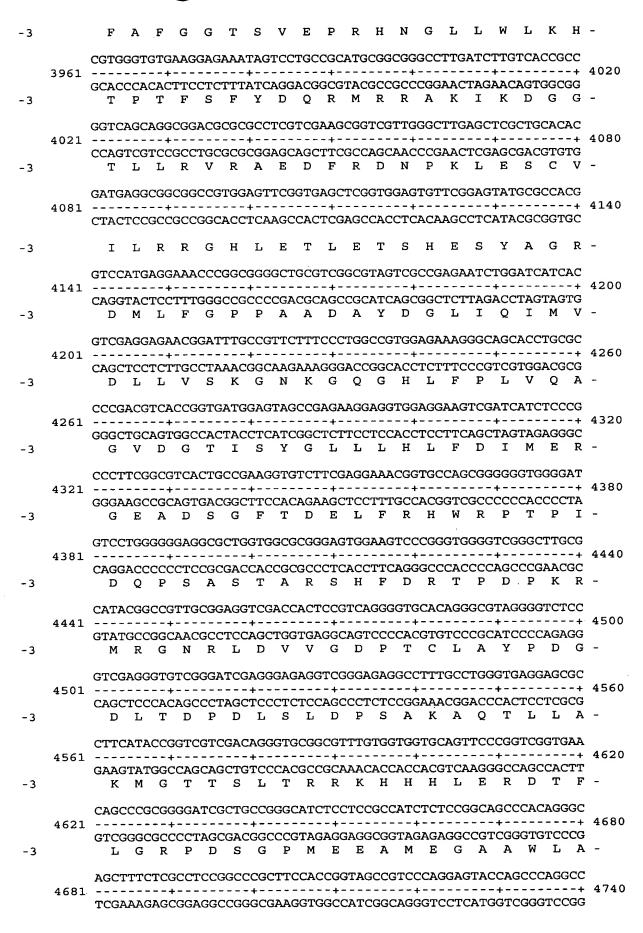
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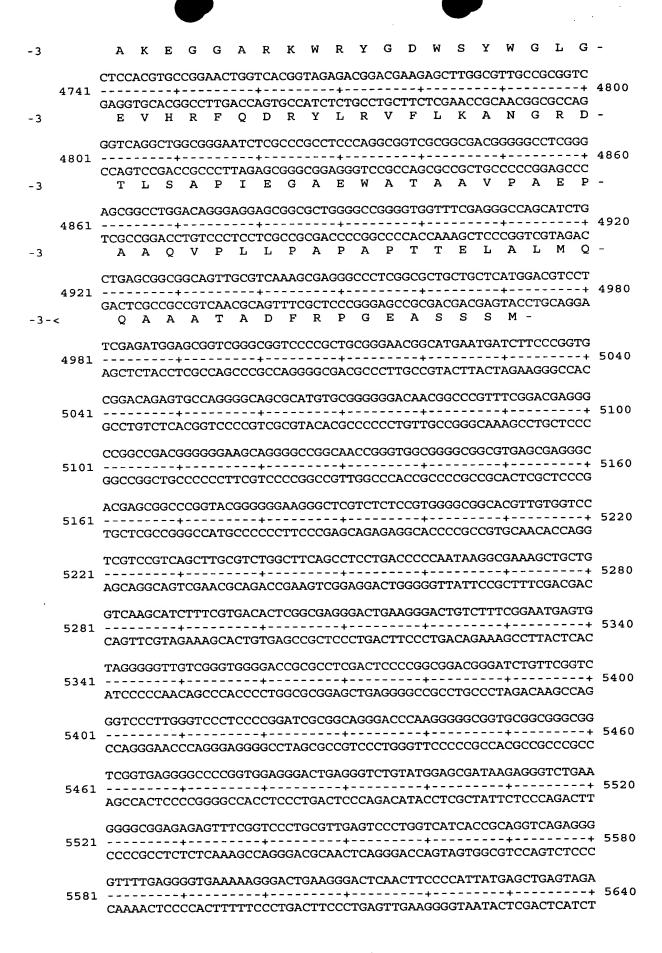
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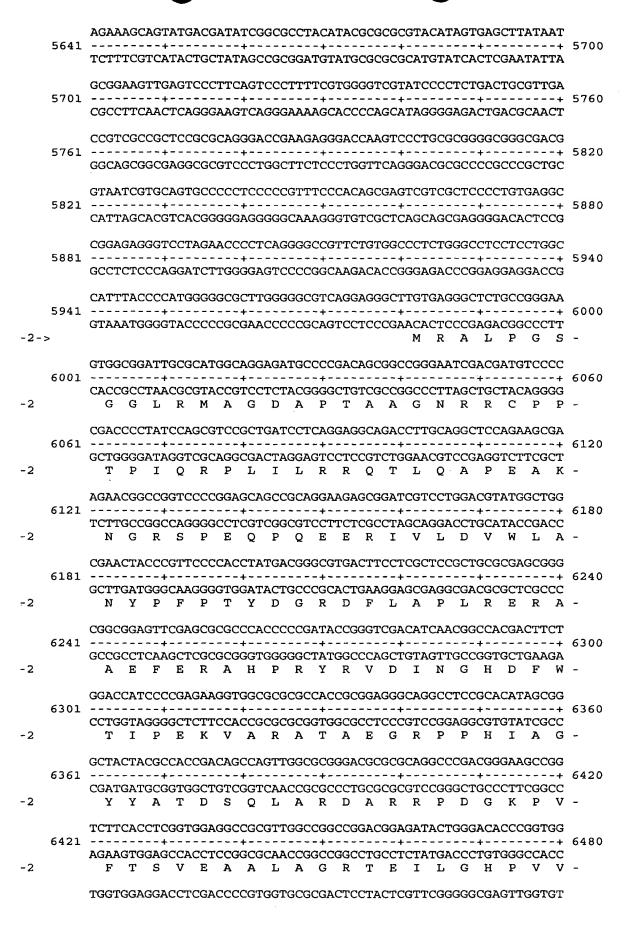
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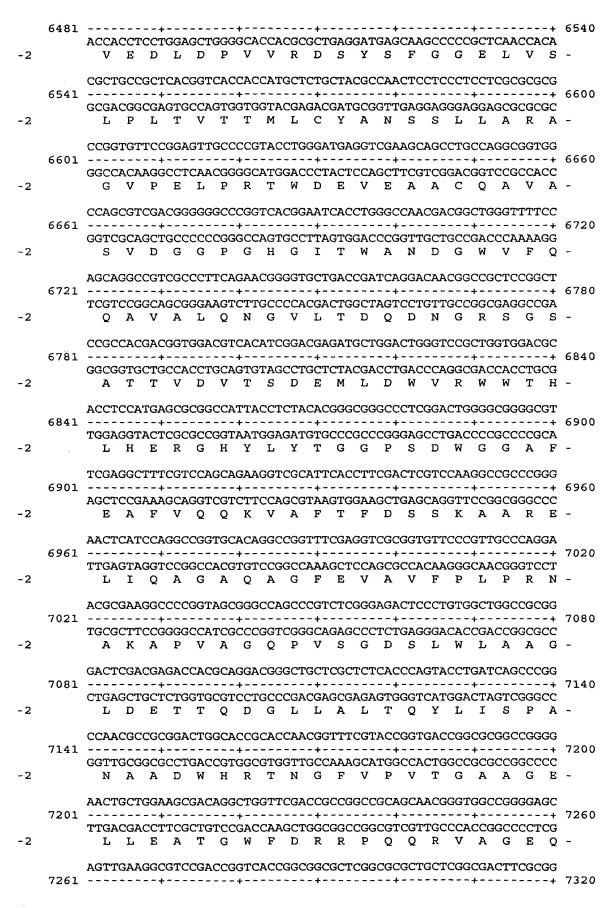
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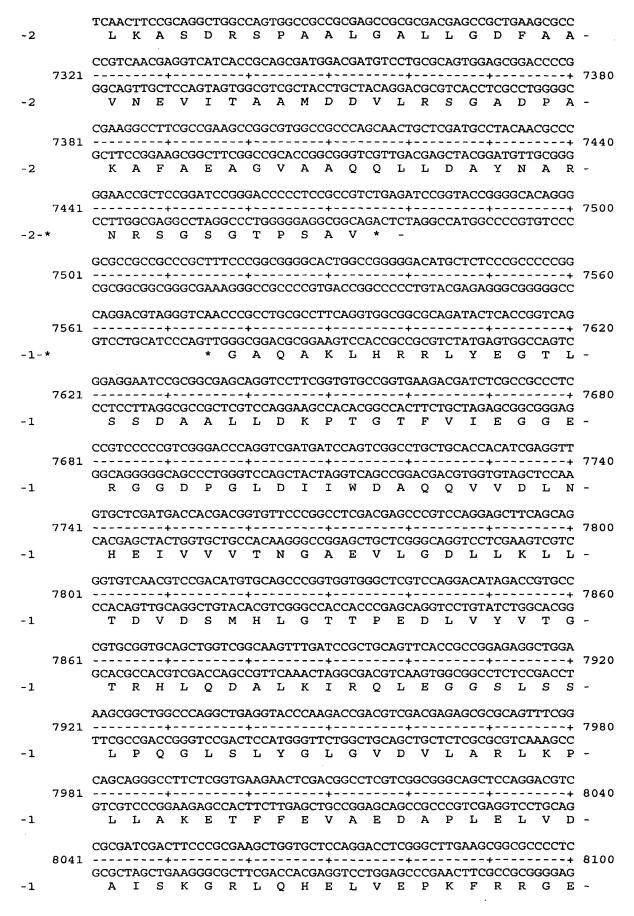
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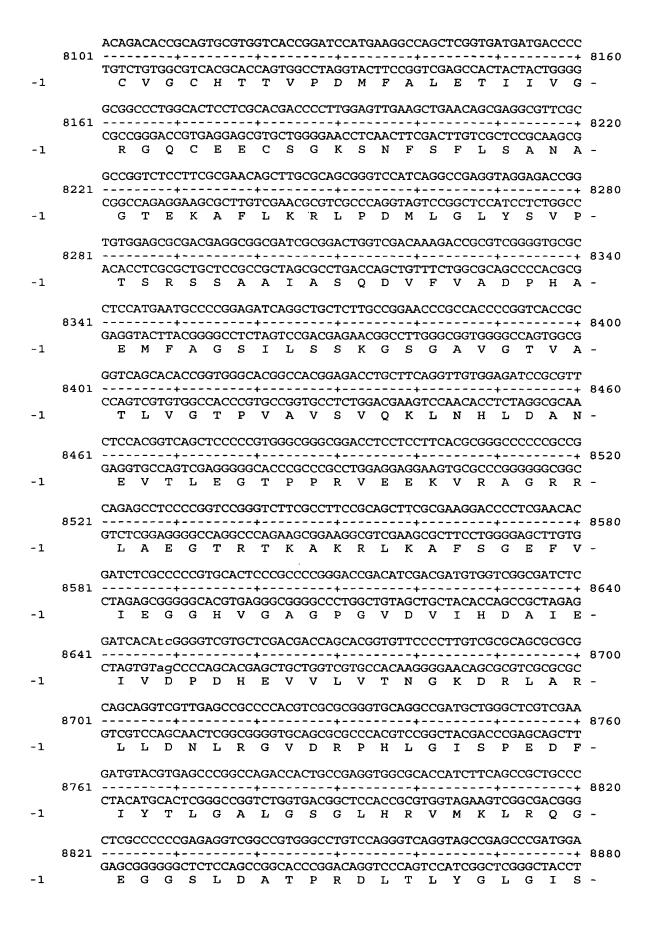
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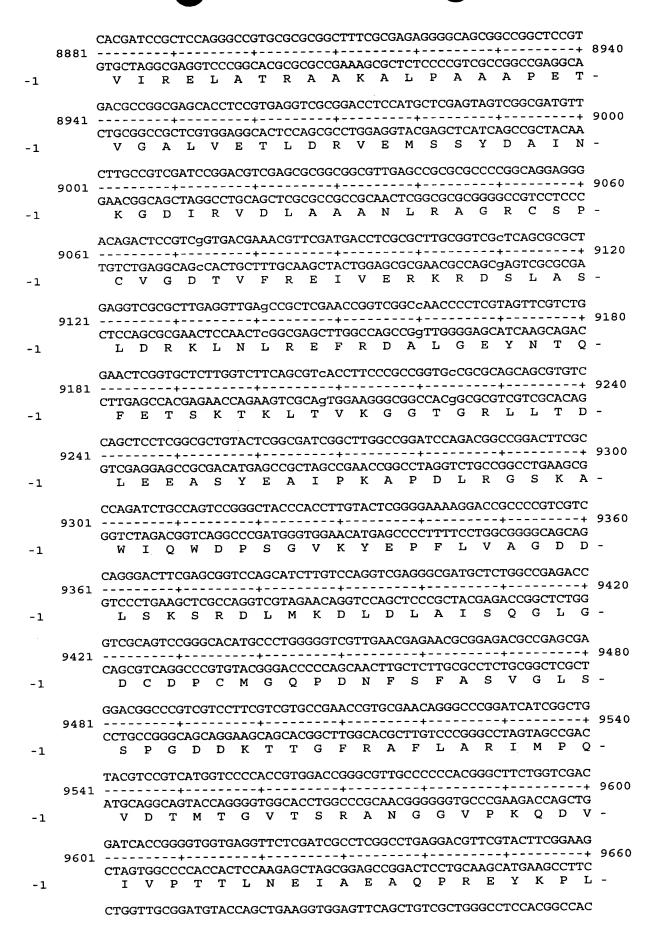


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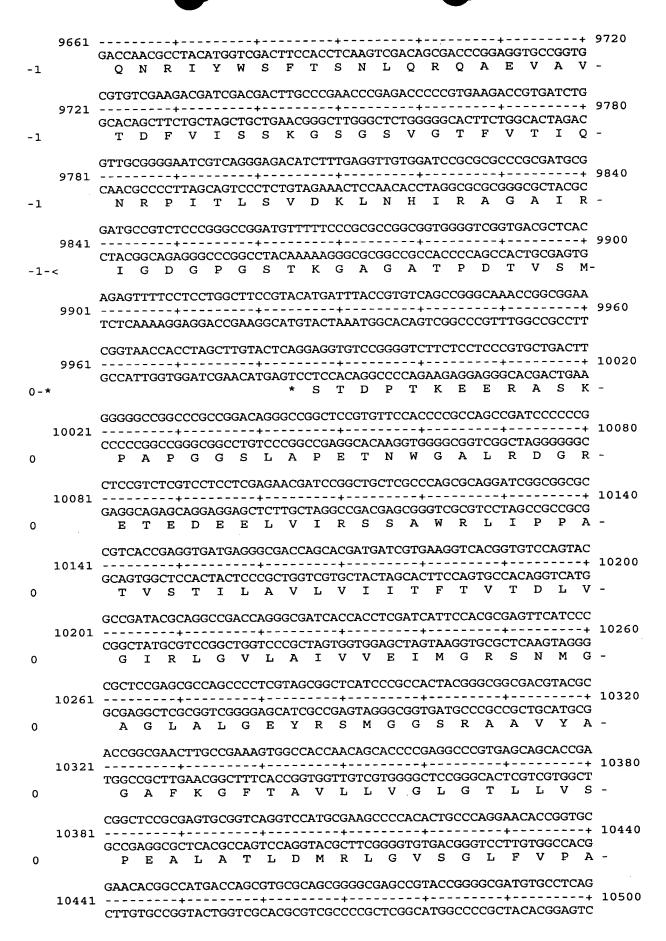
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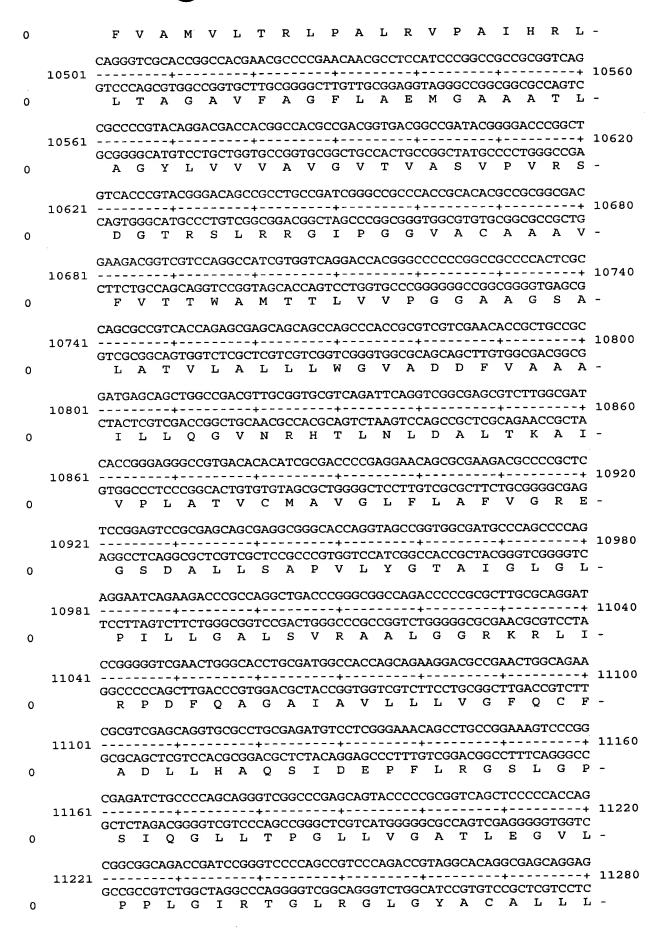
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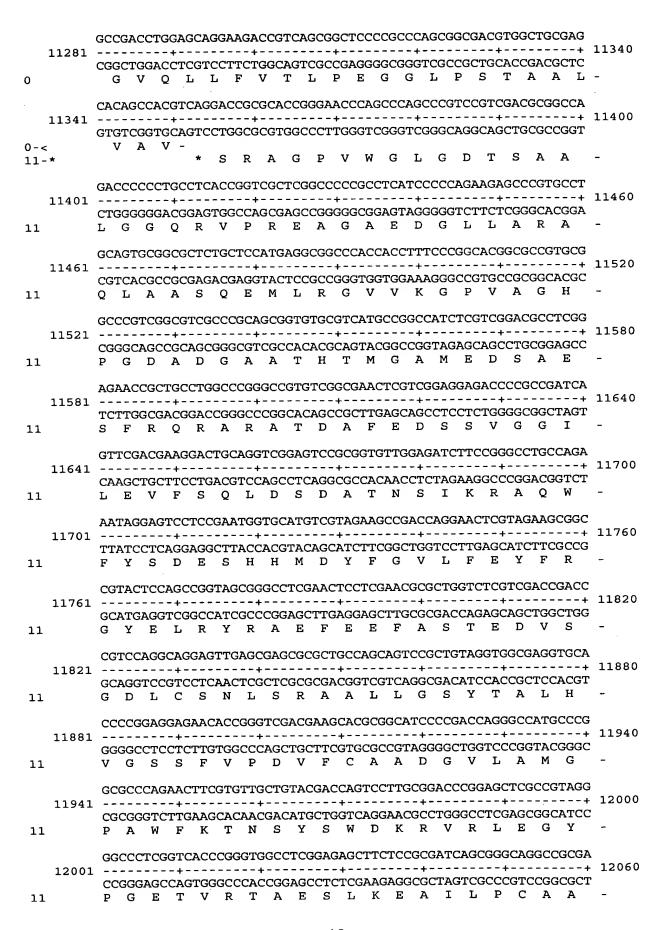


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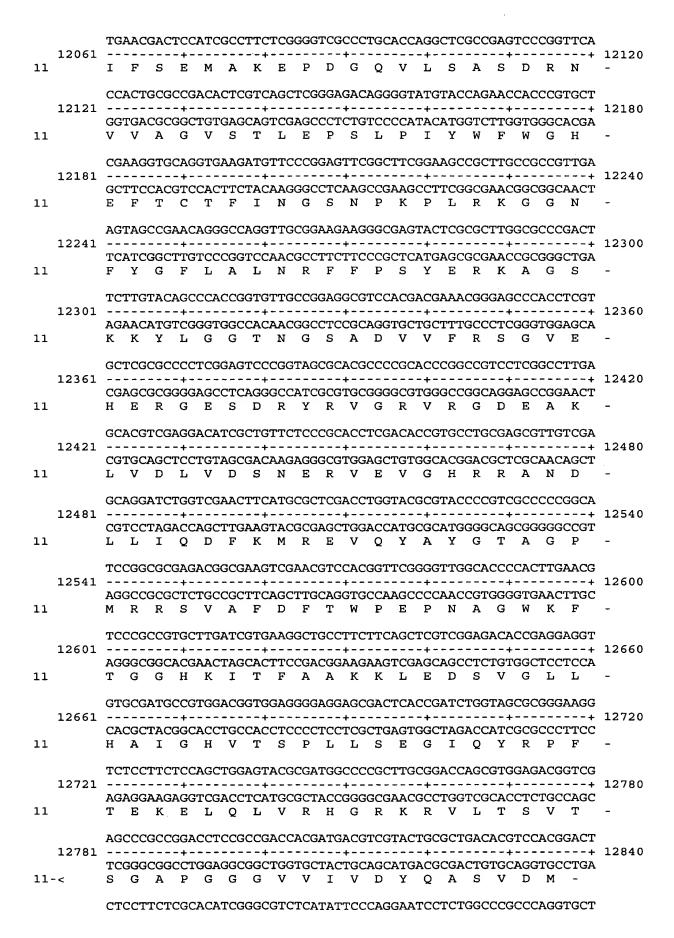
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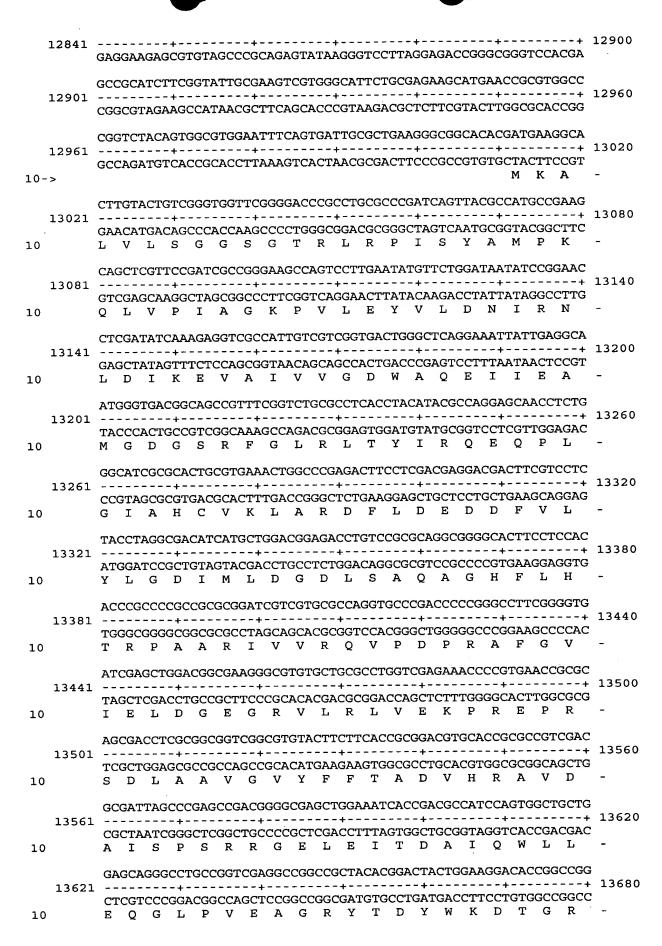
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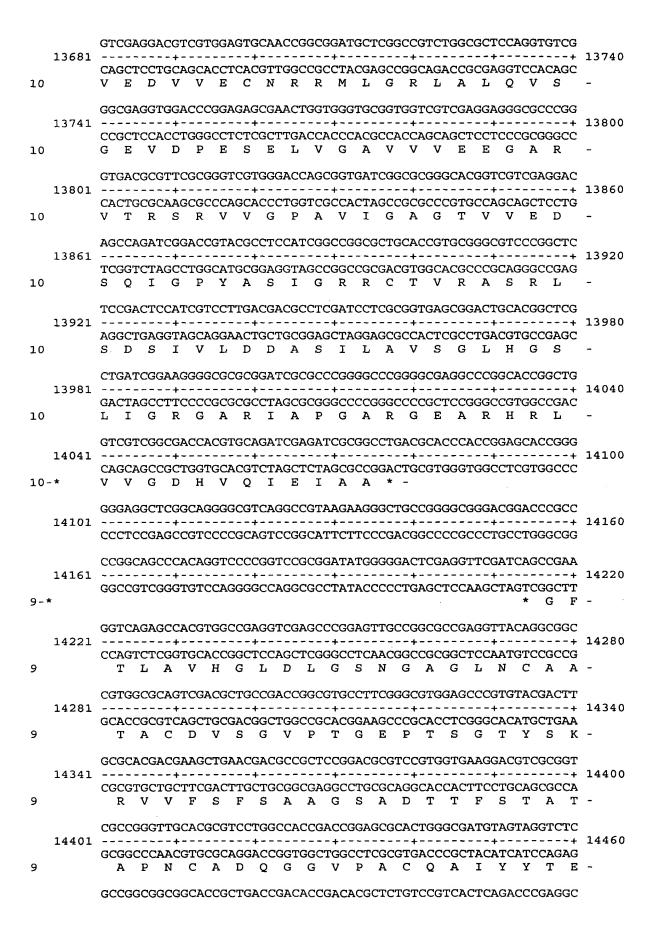
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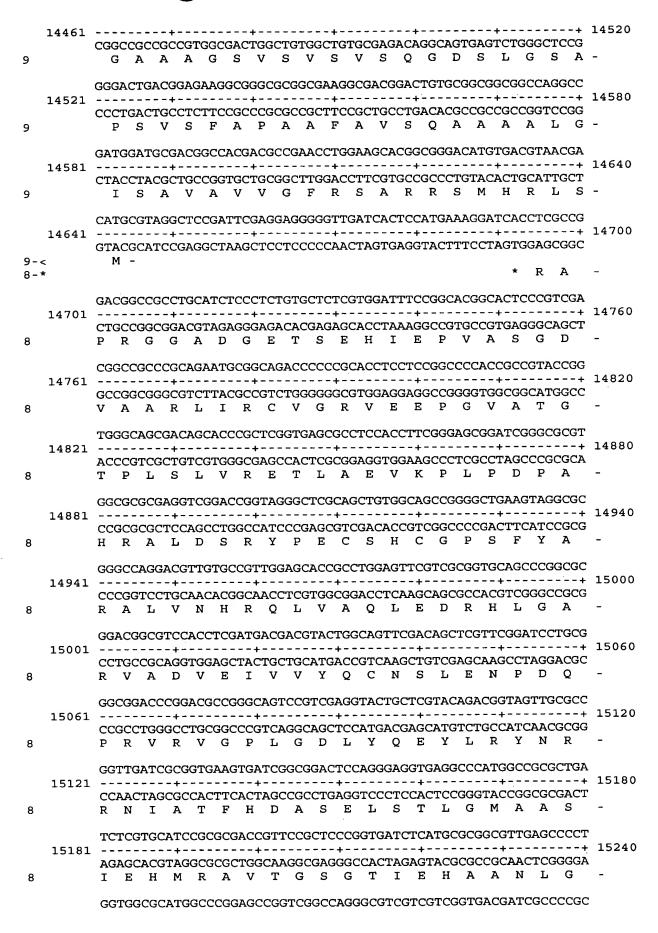


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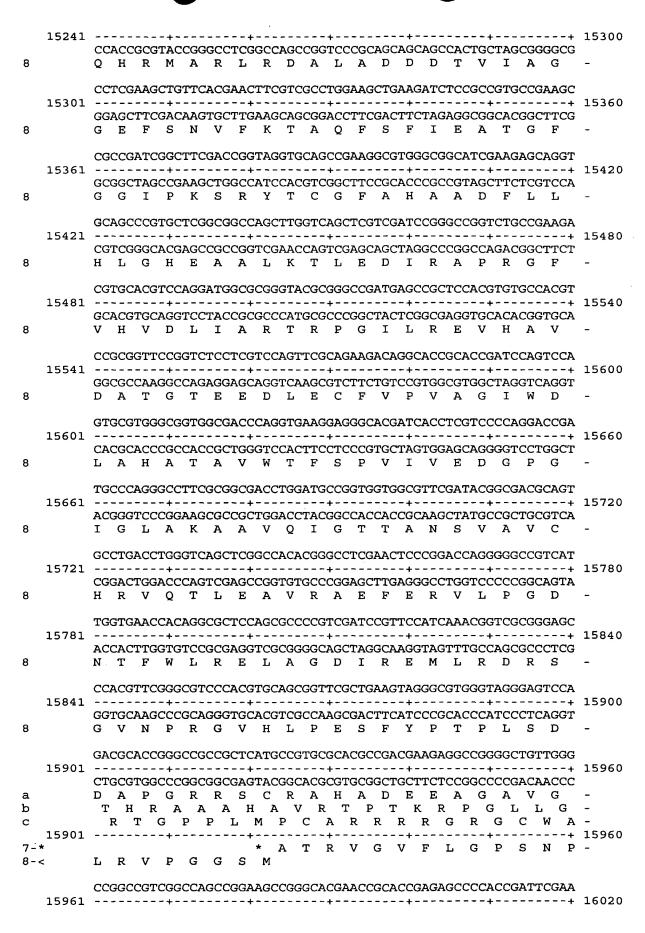
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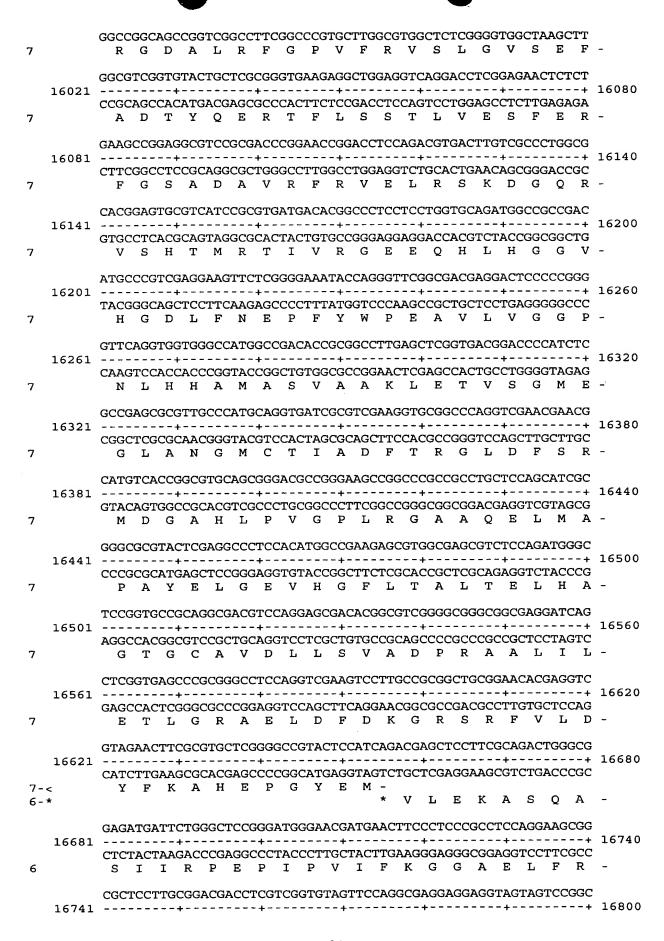


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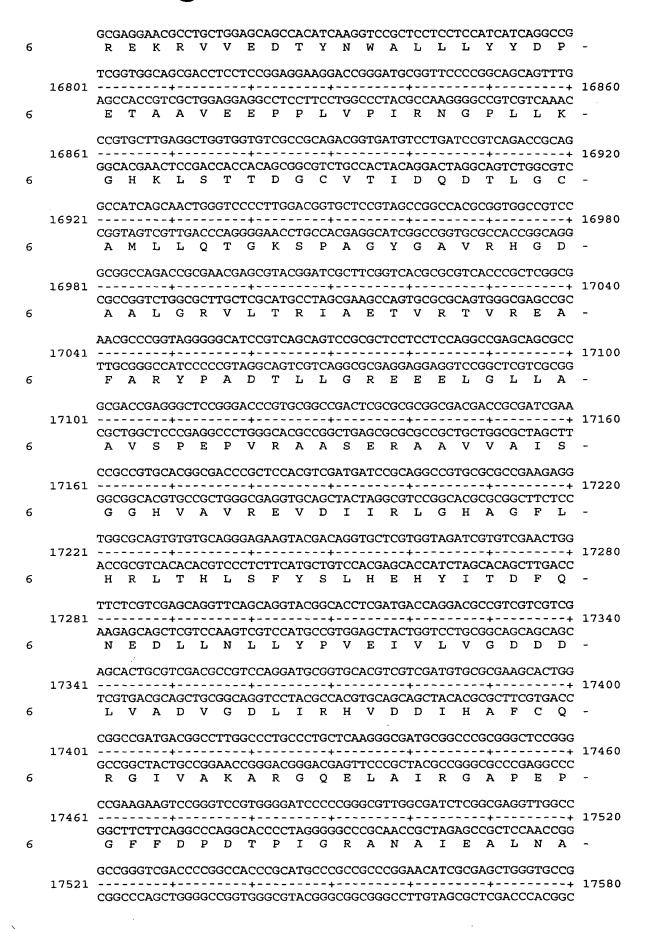
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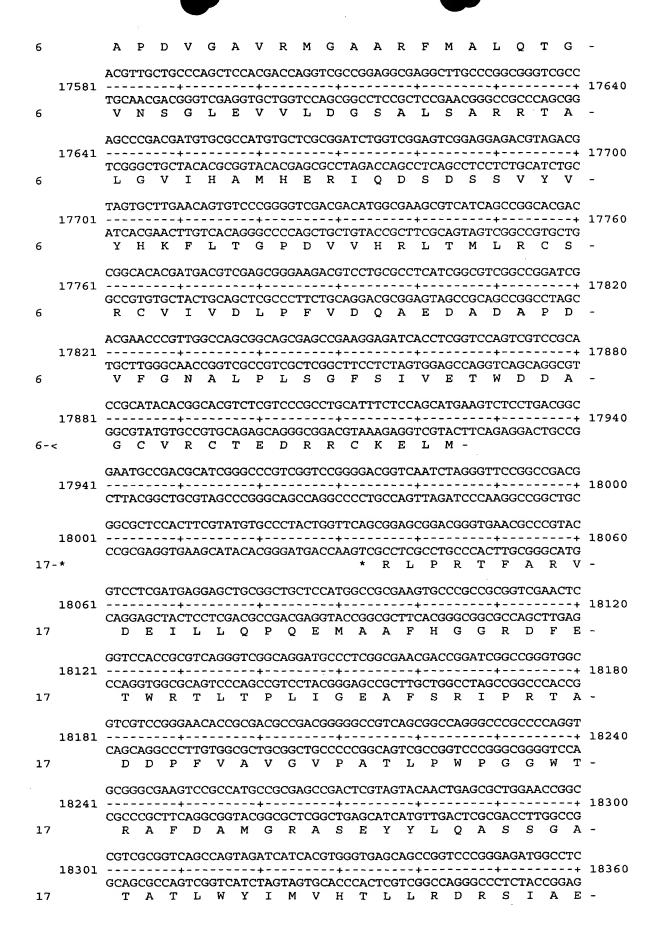
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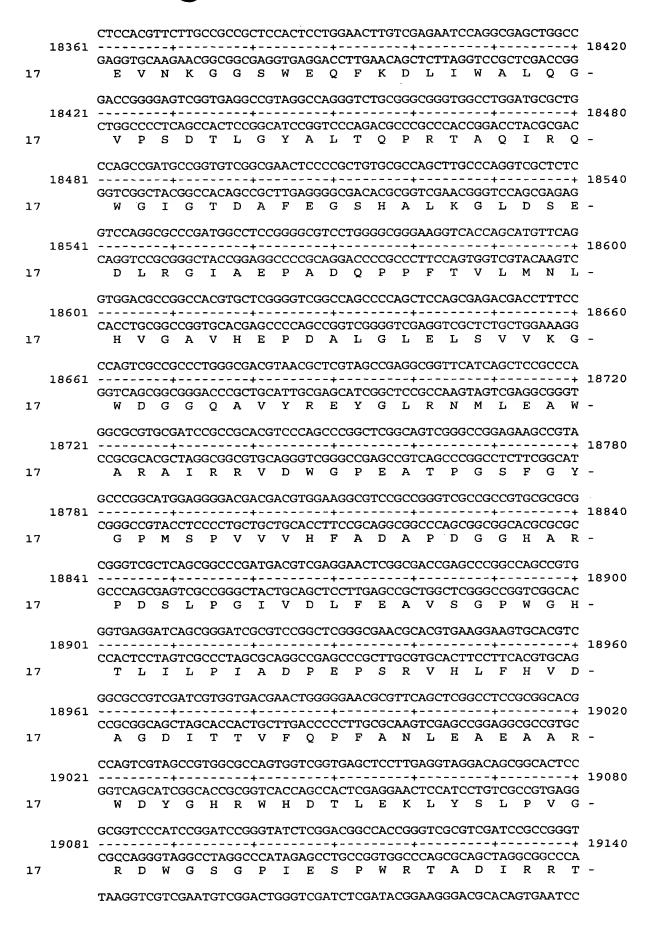


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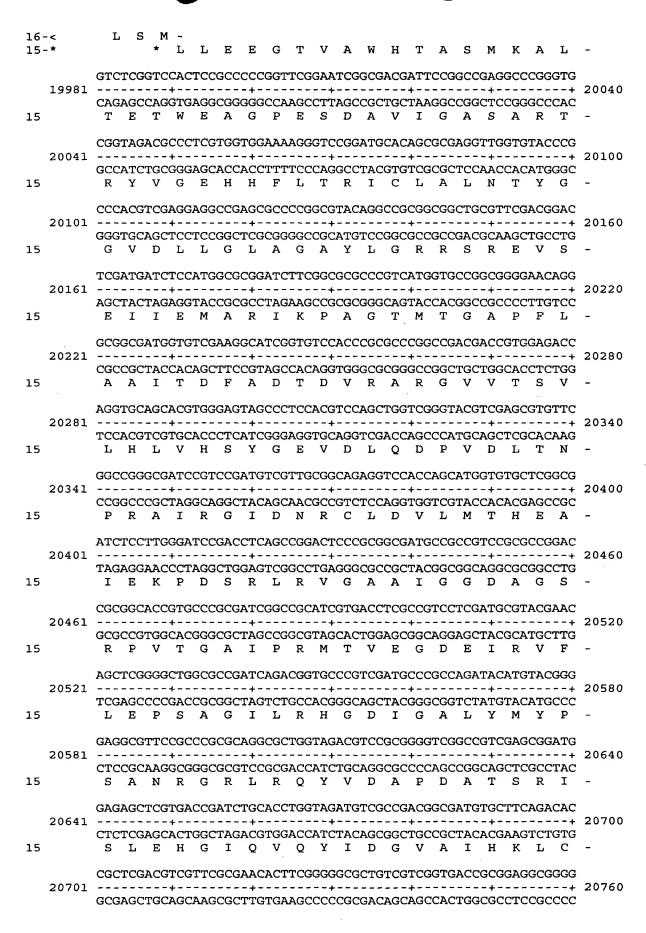


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16	19501	GTGGTAGCGGGTCGCGAAGAACCCCGCGGGCAGCCCGGTGAACACTCCGCGCCCGTCGTG+ CACCATCGCCCAGCGCTTCTTGGGGCGCCCGTCGGGCCACTTGTGAGGCGCGGCAGCAC H Y R T A F F G A P L G T F V G R G D H	19560
16	19561	CGTGATCCGGCTCGTCTTCCCGTGCATGAGATGCCGGGCGGG	
16	19621	GGCGCGGCGACGGCCTGATGCCCCAGACAGACCCCGAGCAGCGGGACCCGGCCGG	
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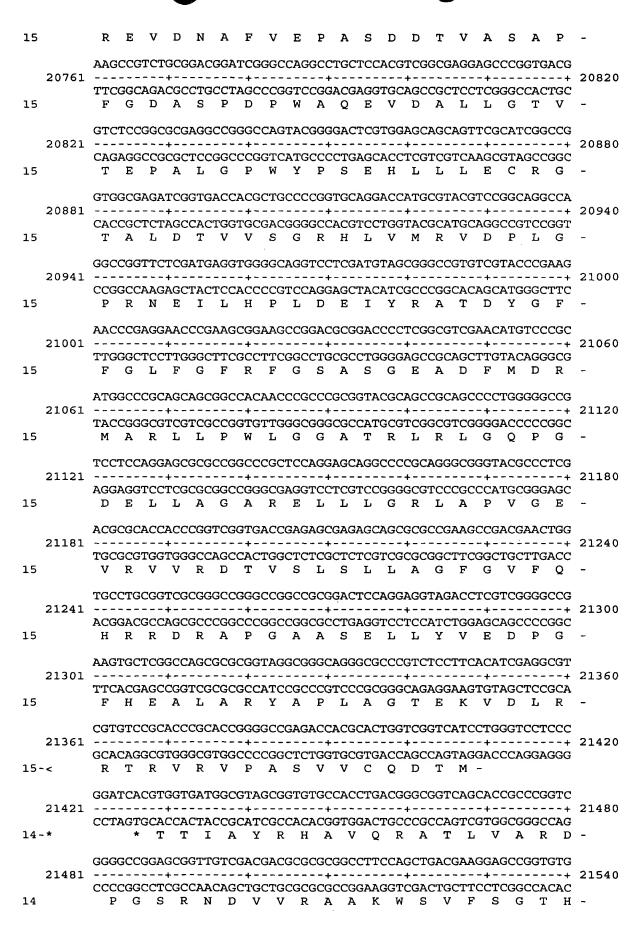


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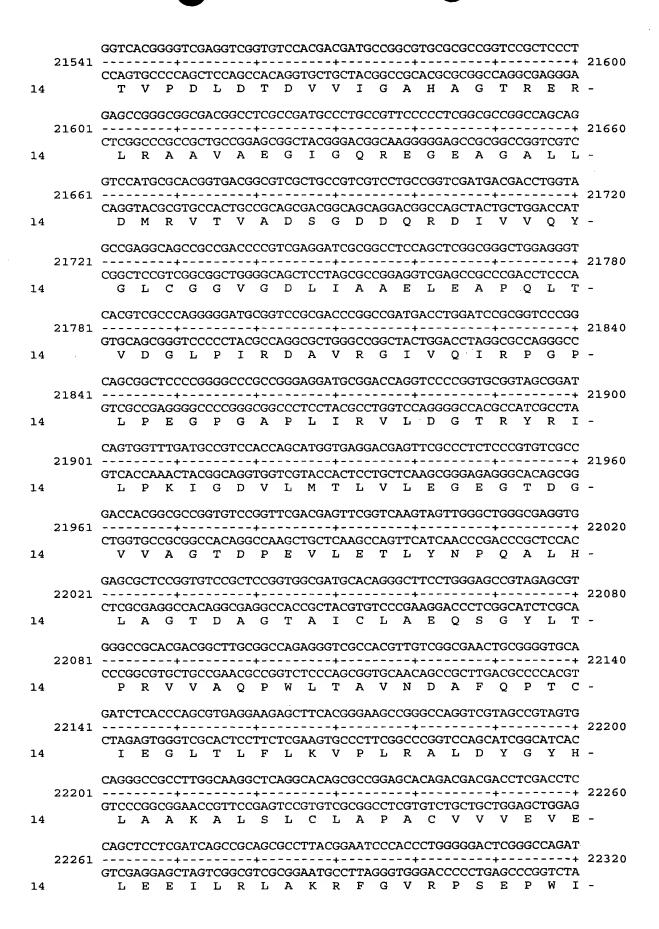
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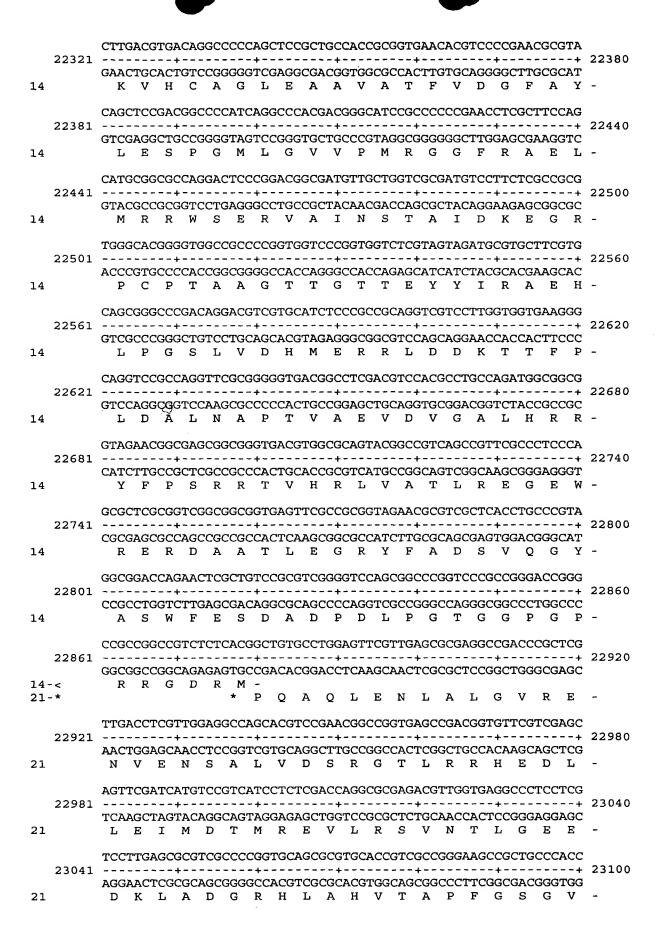
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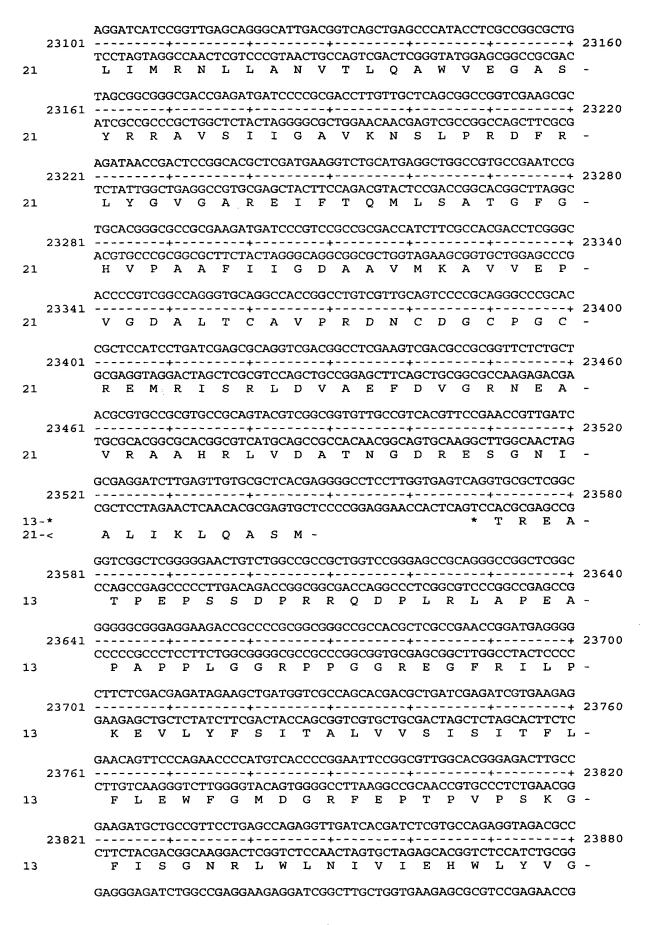
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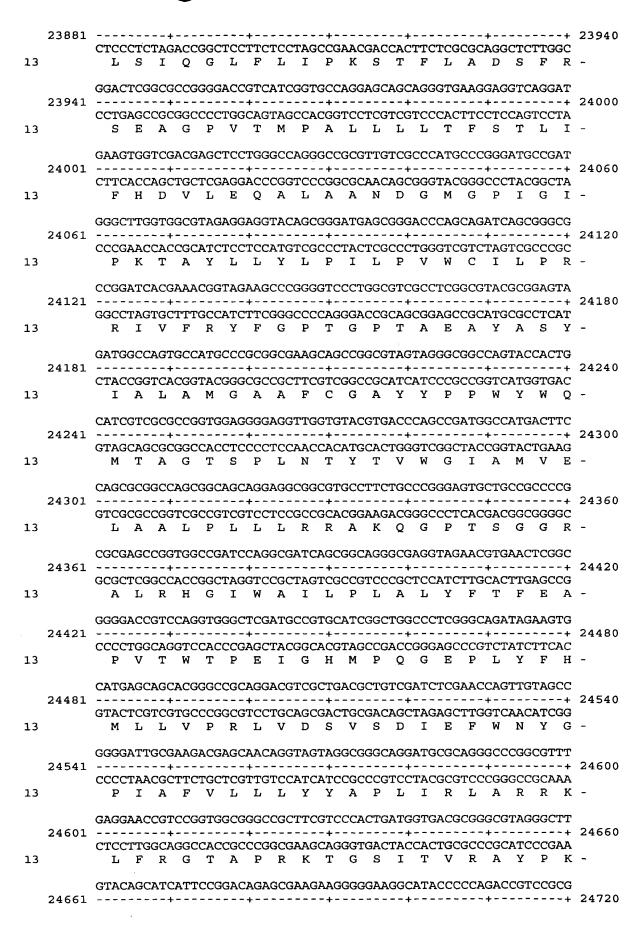
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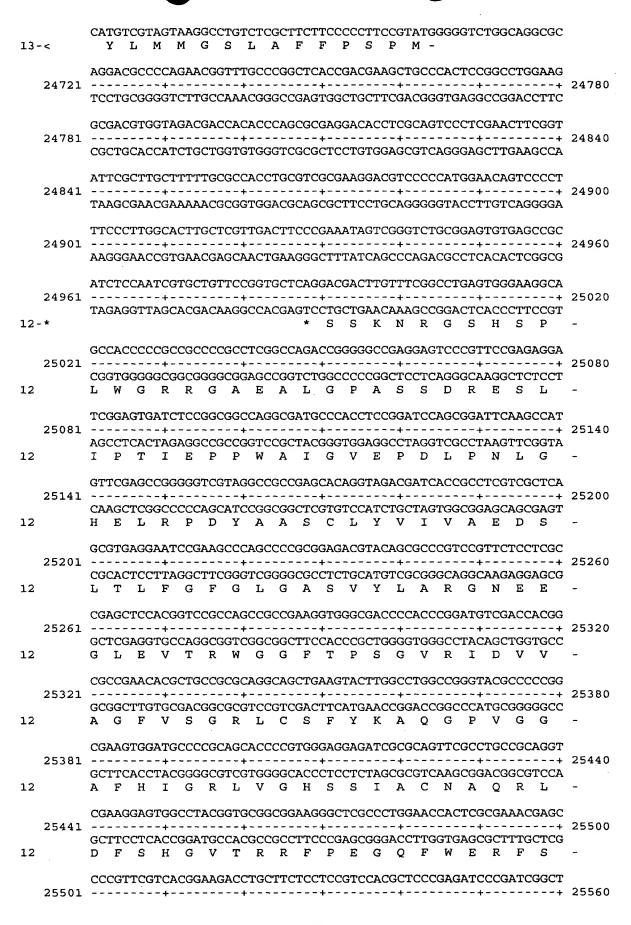
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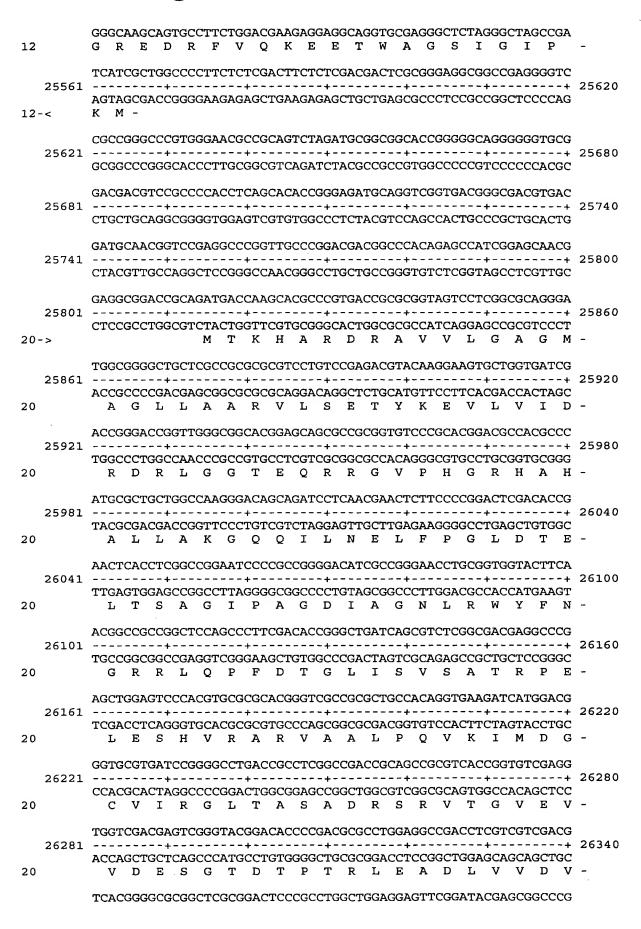


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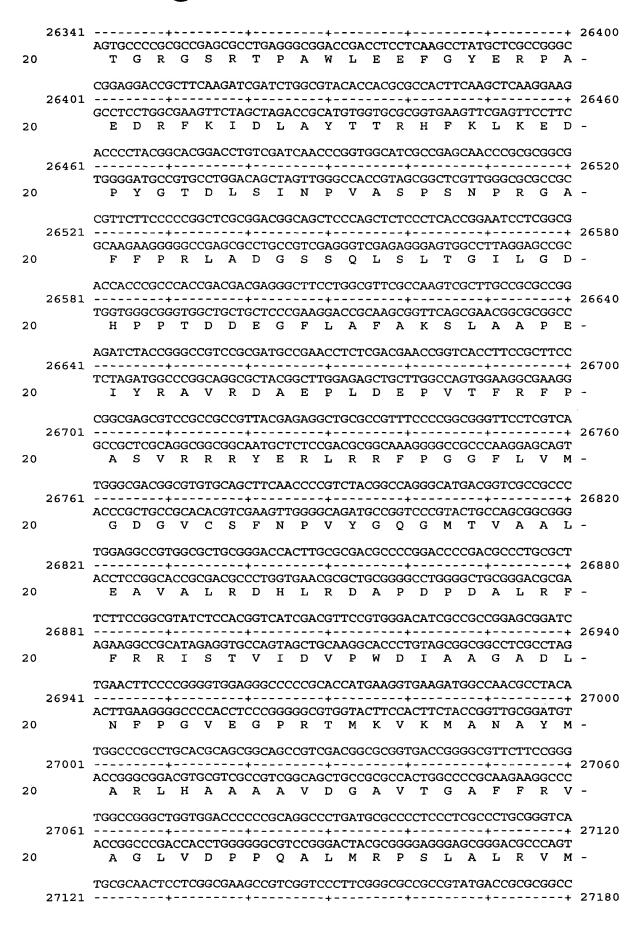




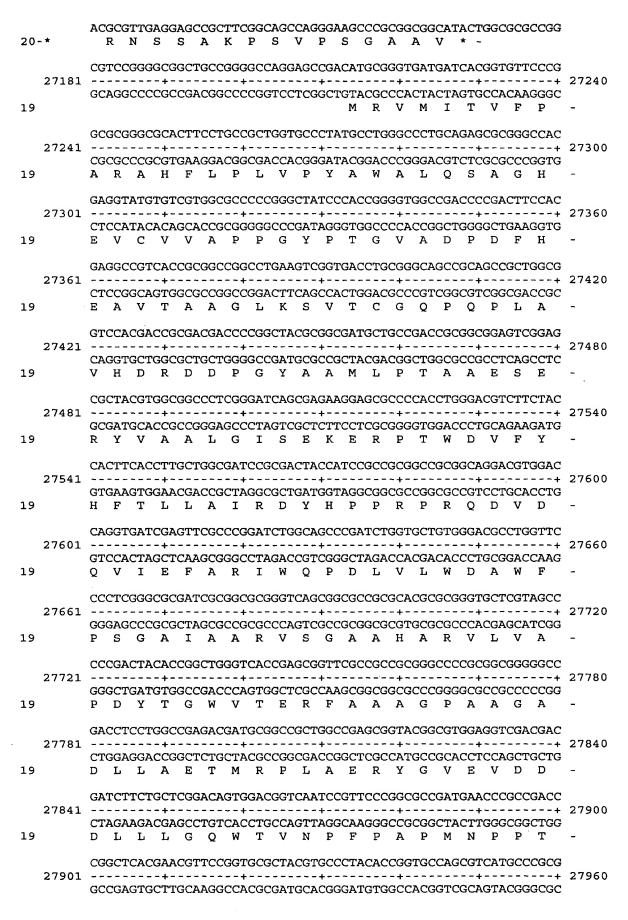
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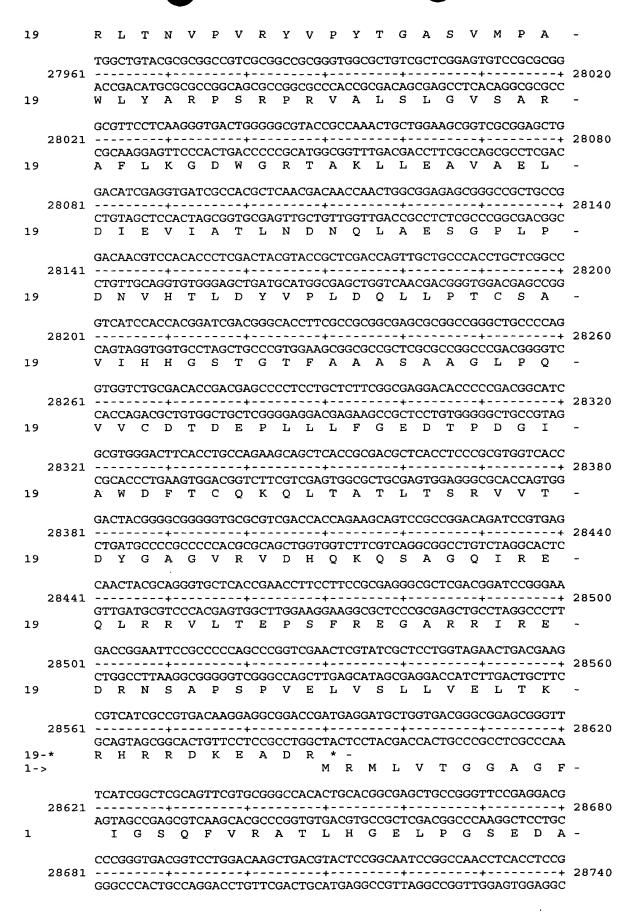


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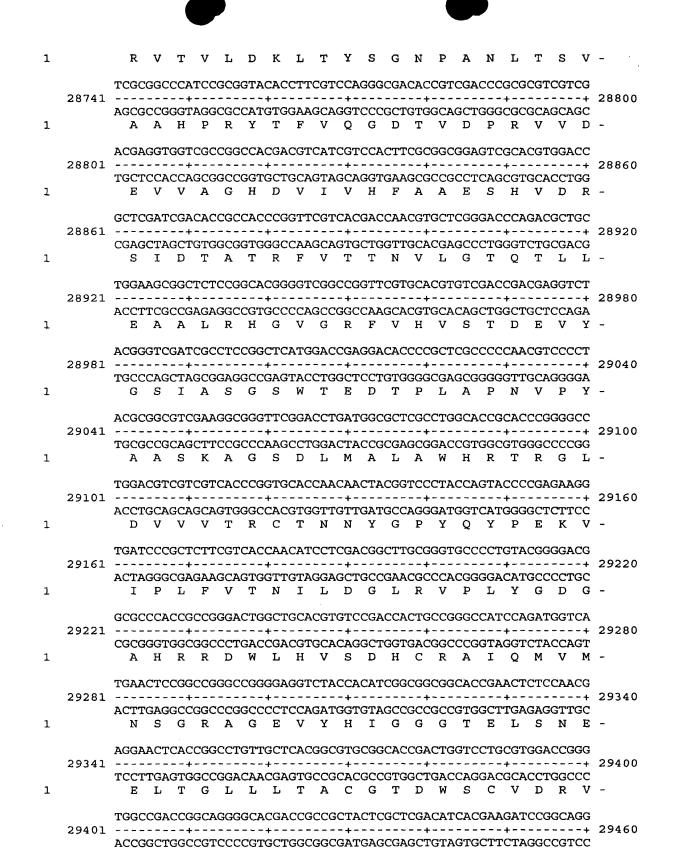


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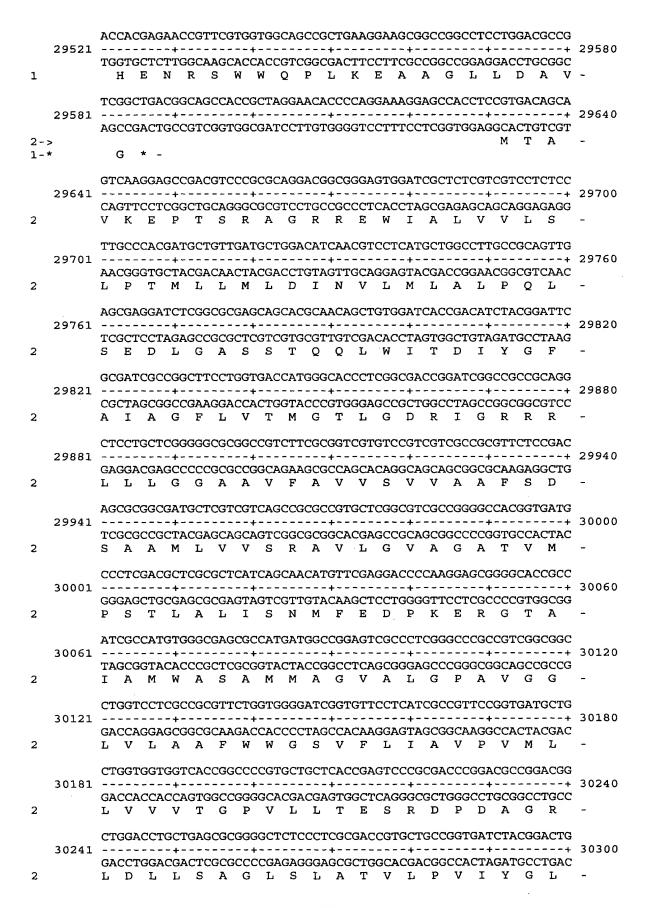
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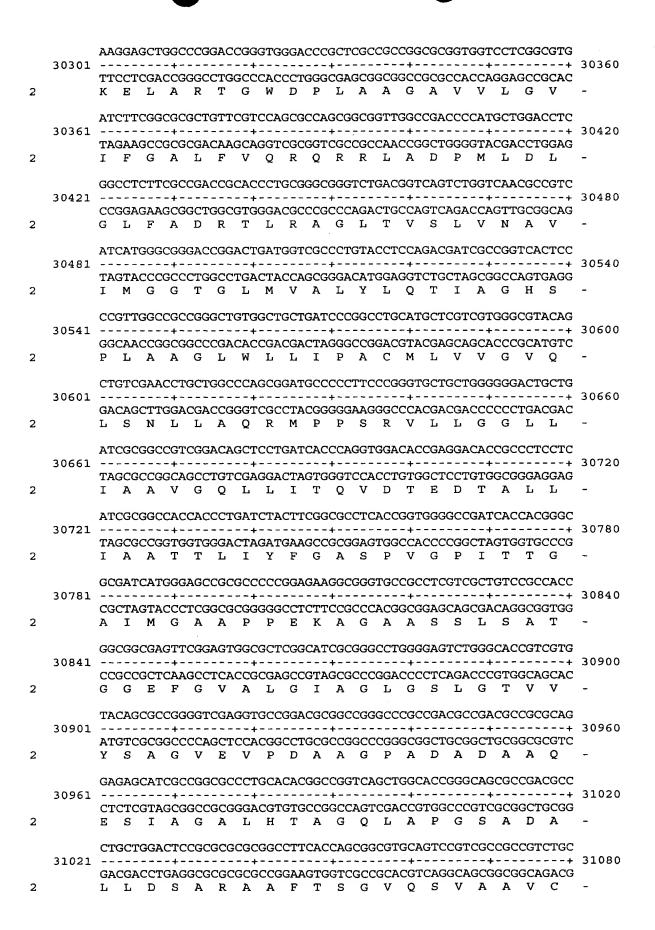


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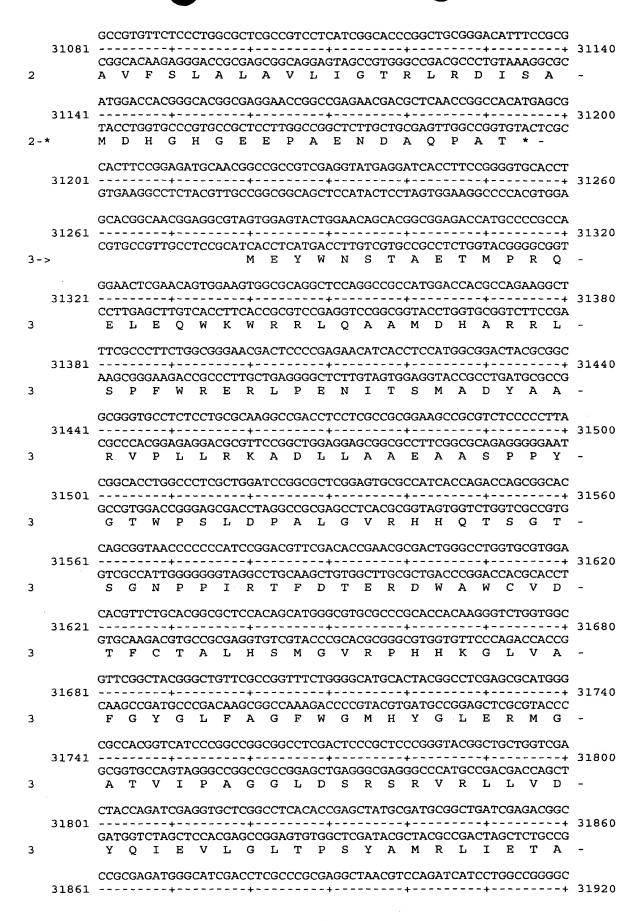
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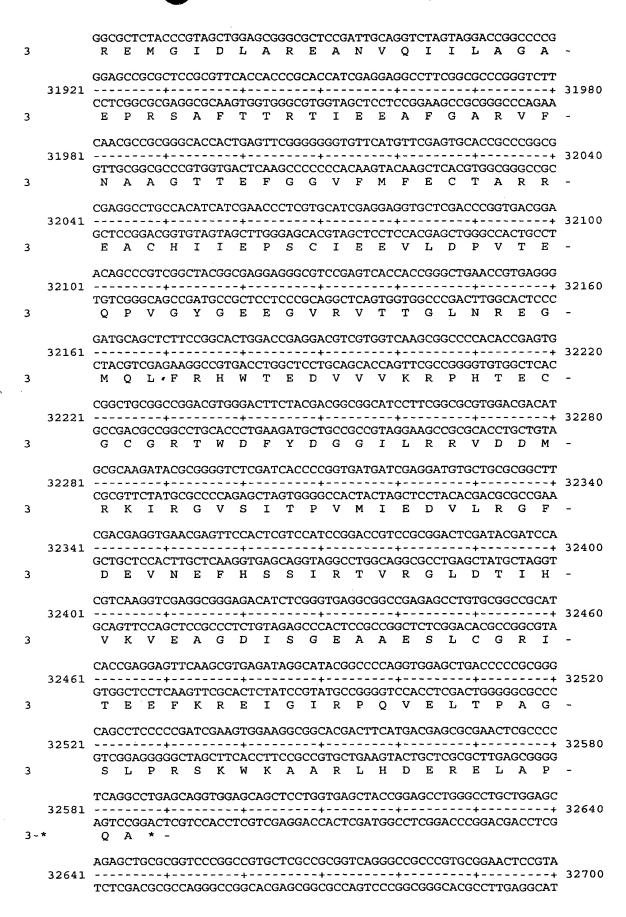
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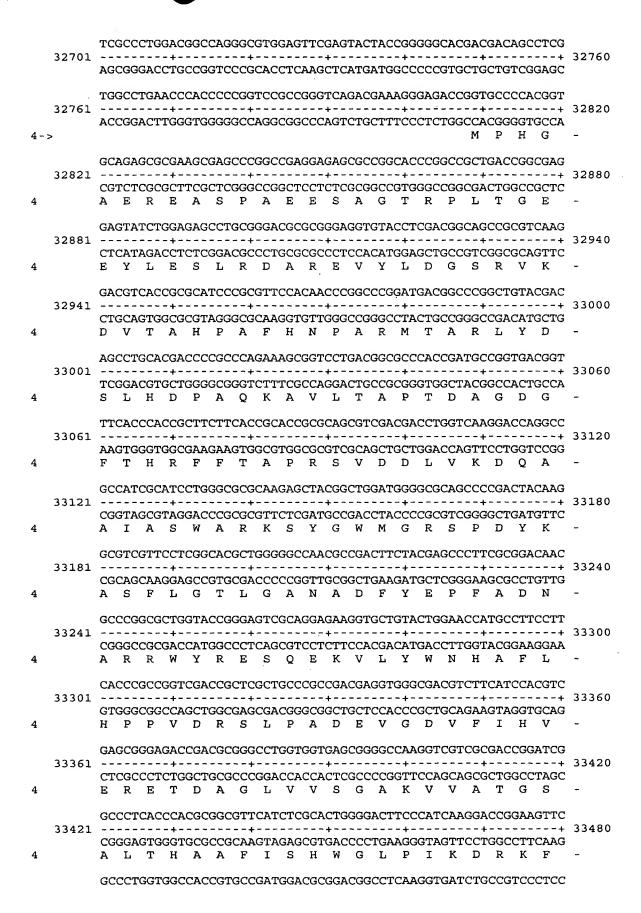
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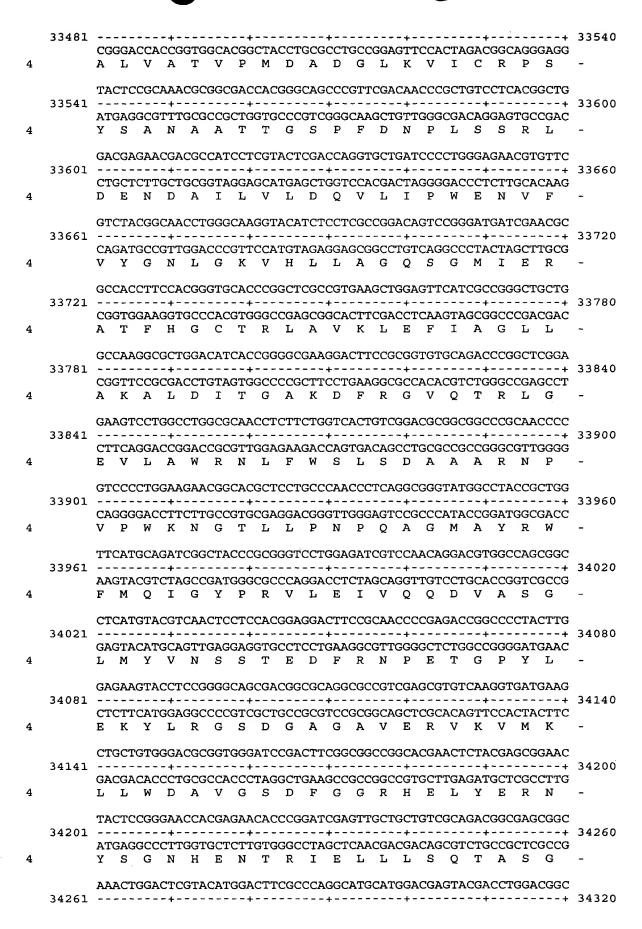


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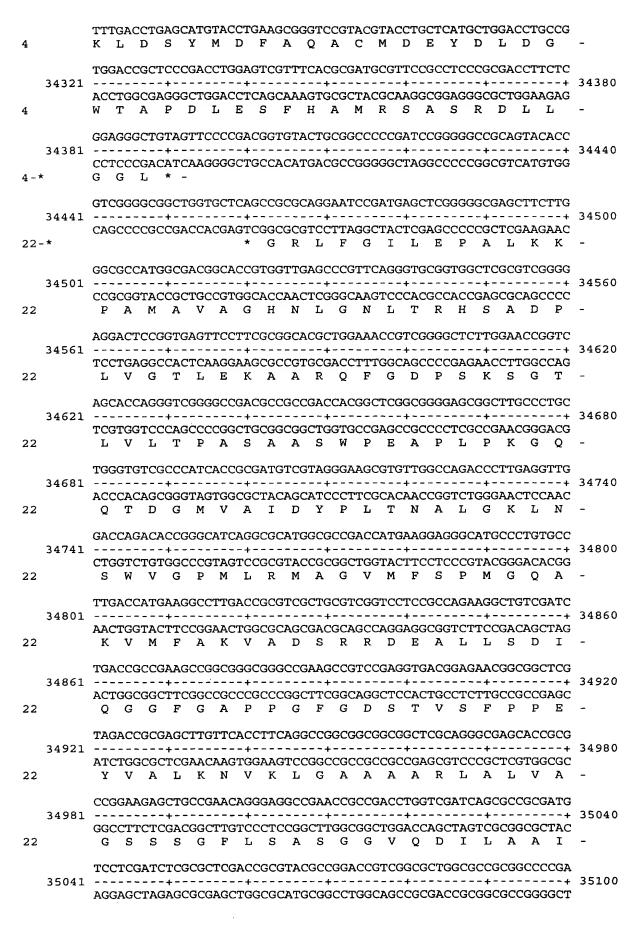


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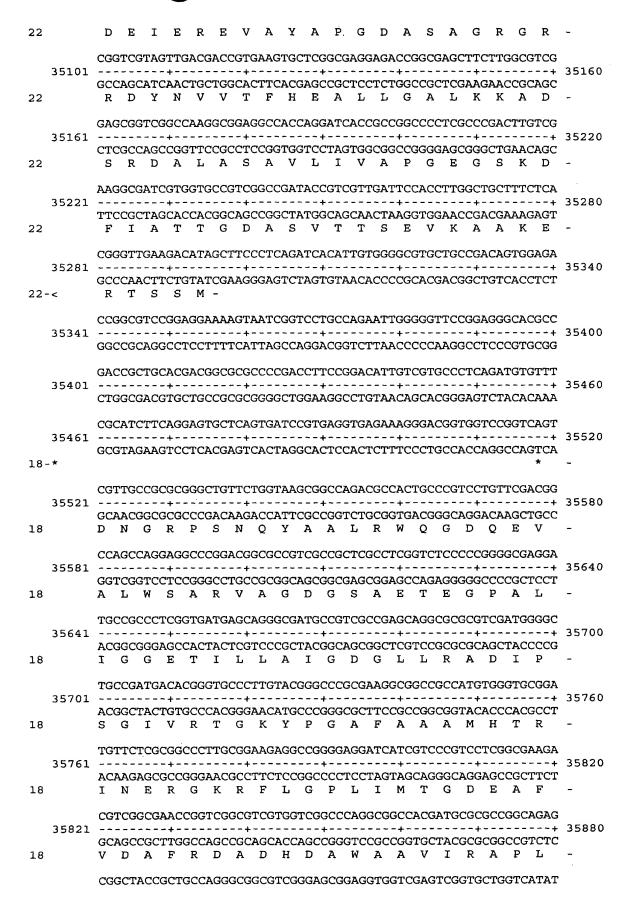




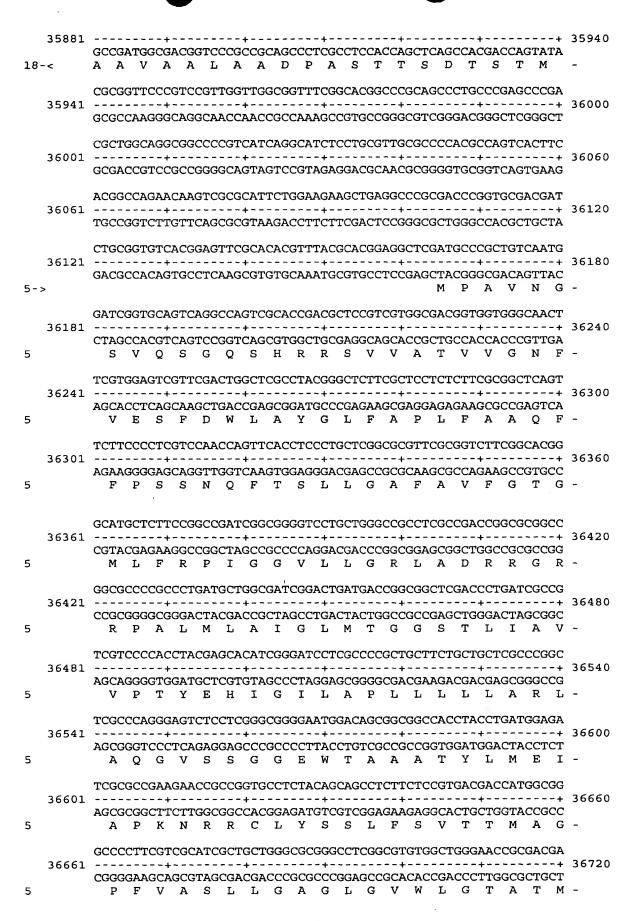
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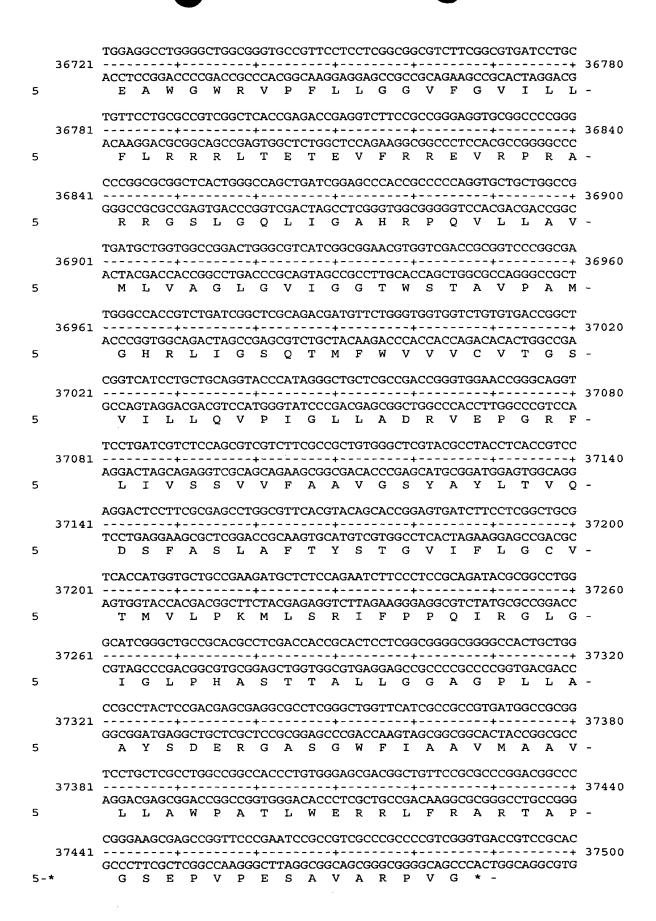






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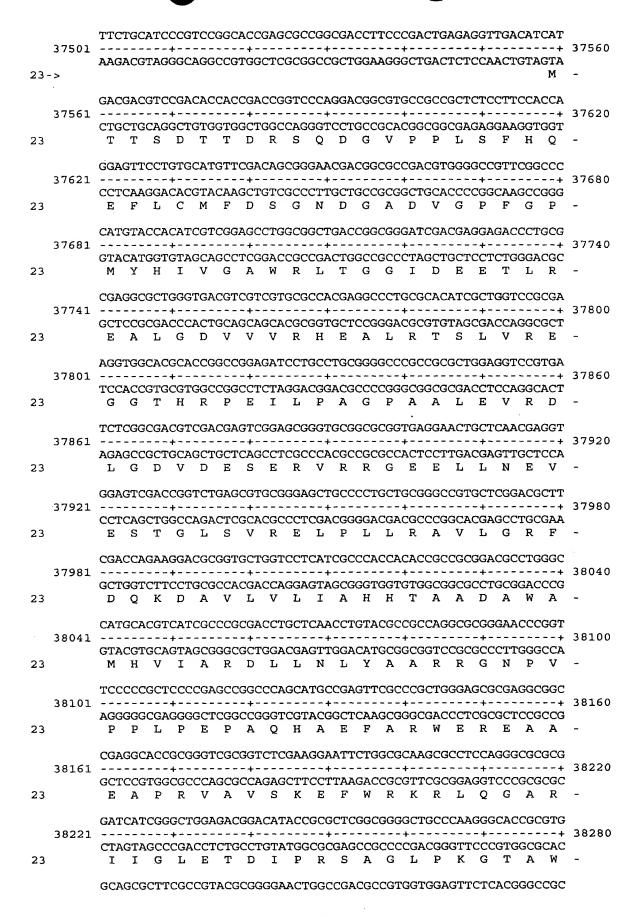




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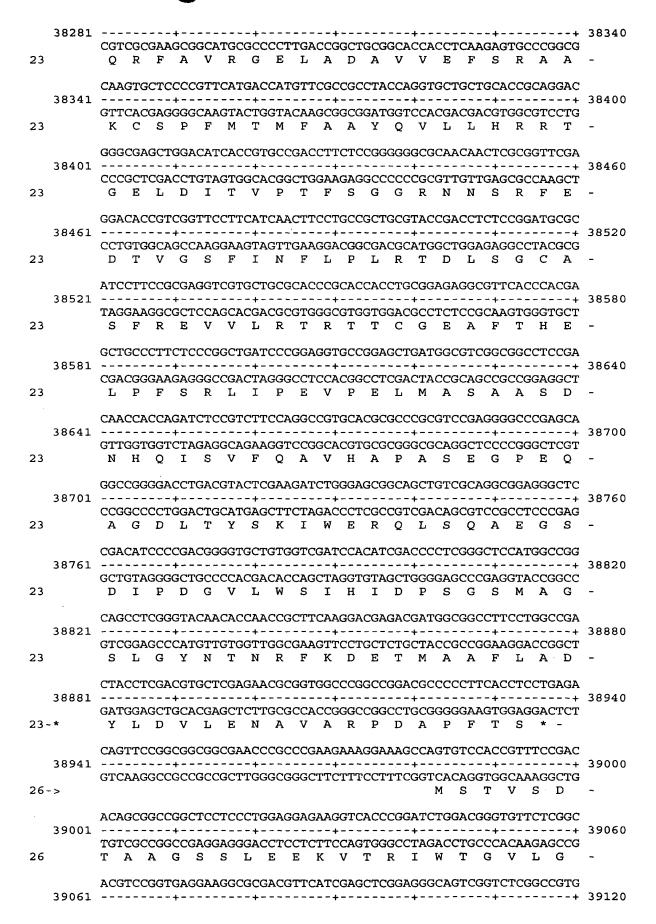
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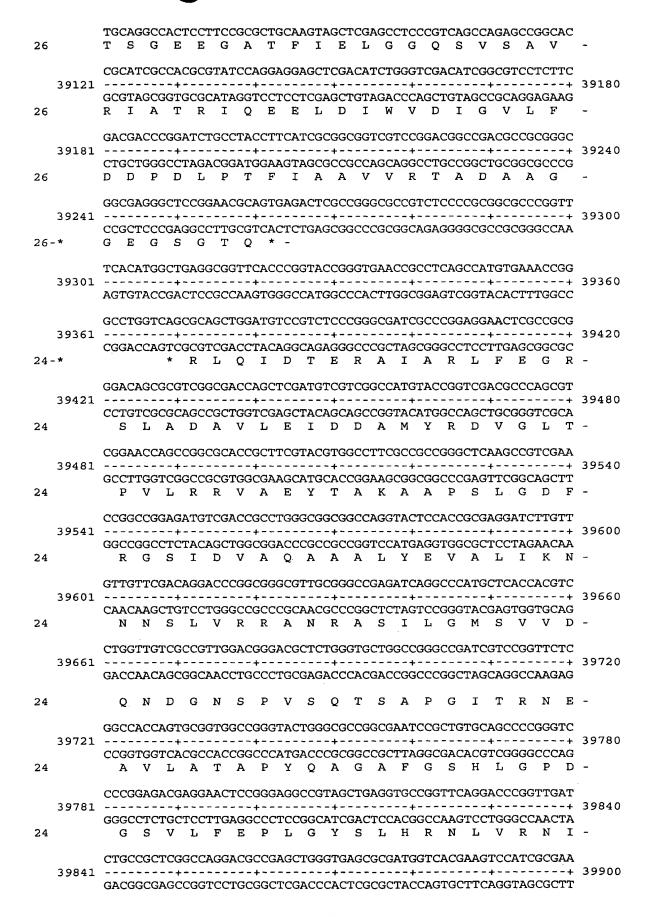


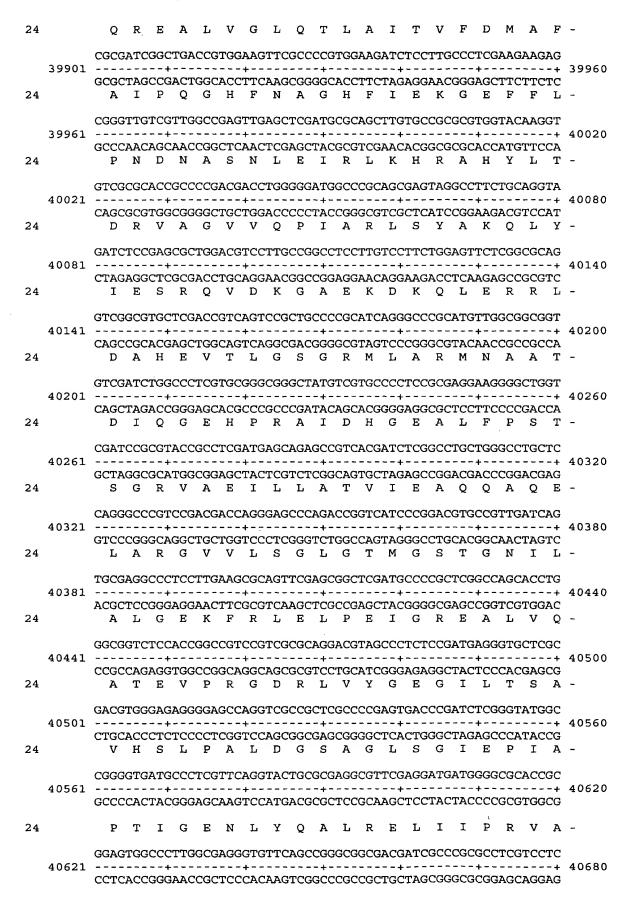




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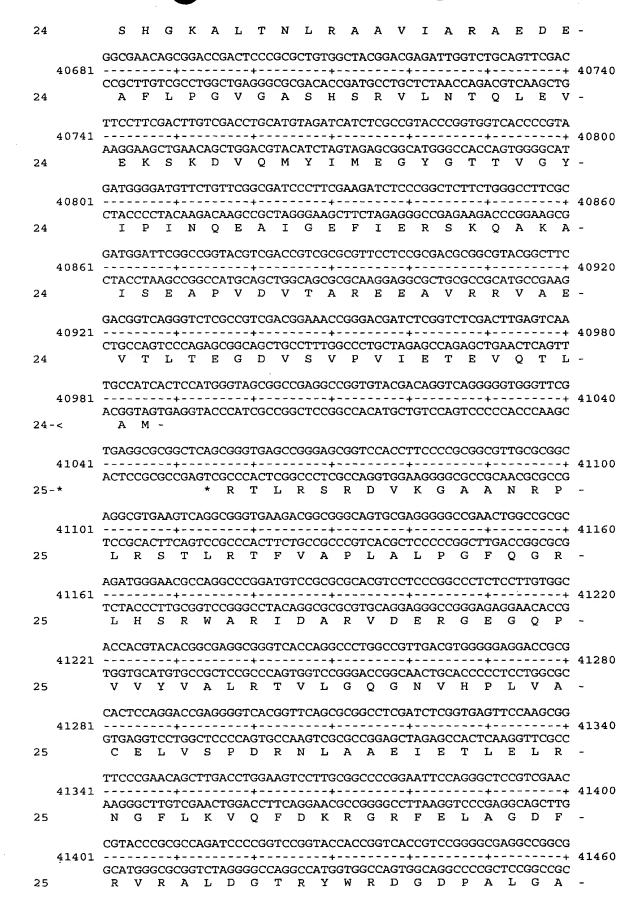


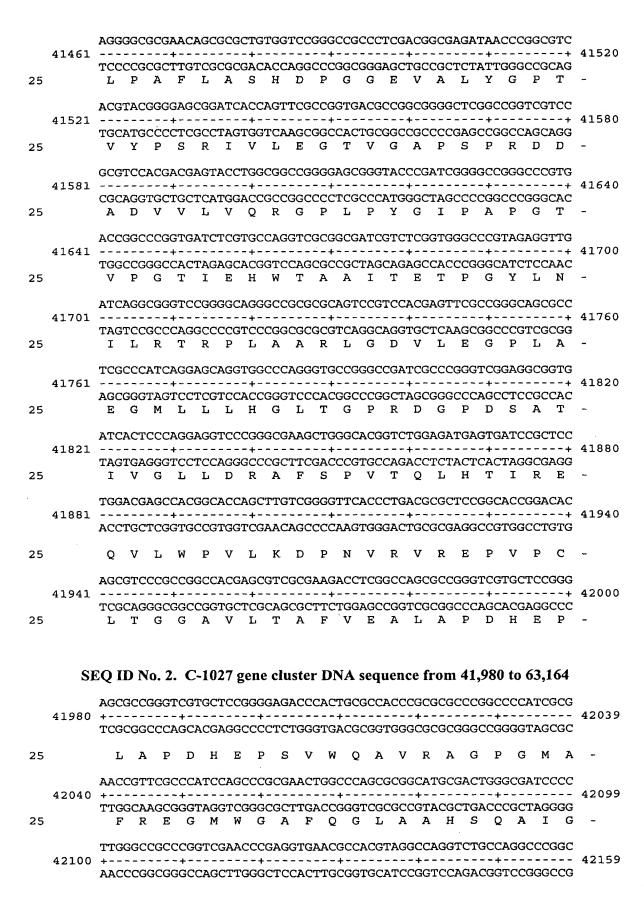














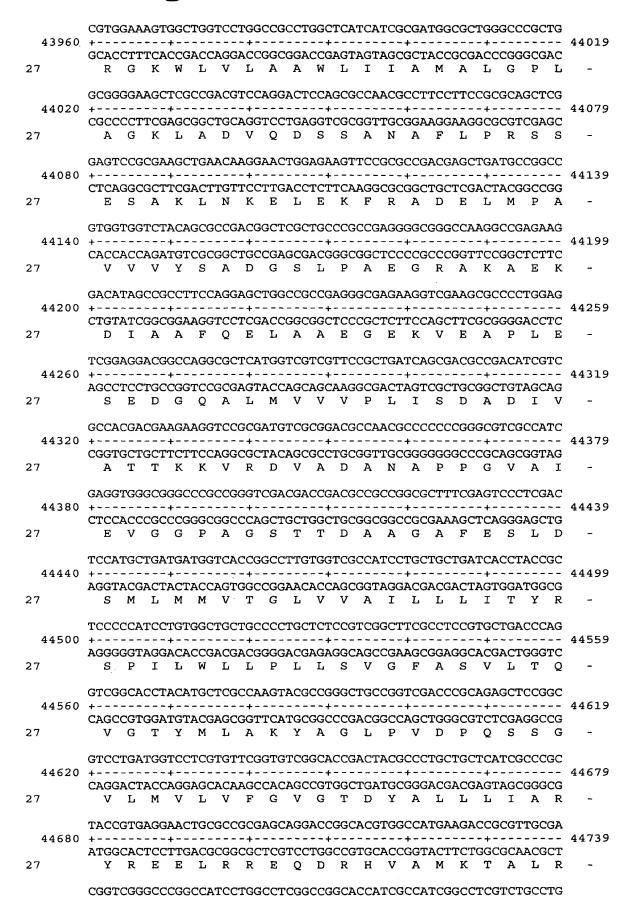


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25		GGGC G	GGC A																		GC A	
	42220	+			+			-+-			+		 -		+			-+-				
25		AGGT D	CGT(GTG(E									.GGA D		CGC(Q		-
	42280																			CGT		
25		AGCG D																		CAA(R		-
	42340	CCCG																				42399
25		GGGC	GCG	GCA(GGC(CTC	GCT'	rgg	TGC	GGT(CCA	CCC	GCG	GGC	GGA	GGT	CCT	'GAG	GGT		CG	-
	42400	ACCG																				12150
25	12100	TGGC		AGG	CCG	CCC	GCG(GGC	CGA	CGT	AGG	CGT	GGC	GGT	GGC	CGC	TCG	GCA	CGG		ЭC	-
	42460	CCGG																				42E10
25	42400	GGCC		GCC	ACT	CCC	GC.	rcc		GCG	CCC	GGC	GCA	.GGC	GCC	AGT			GCC.			-
	10500	TCGG																				40550
25	42520 I	AGCC	GCA'	TCG				ACG		GCT'		TCT	GCC		GTG				GGC	GCA		425/9
		CGGC																				
25	42580	GCCG R R	CCT	GGC'	rcc	GCA	CGT	GGC	CGG	CGC	AGT.	ACA	GGG	GCG								42639
	42640	GCGC																				42699
	12010	CGCG																				12000
	42700				+		- - -	-+-			+				+		- 	-+-				42759
		AGGC																				
	42760				+			-+-			+				+			-+-				42819
	42820	TCCT	_		-									-	-				_			42070
	42020	AGGA																				42013
	42880	ACCT																				42939
		TGGA																				
	42940	CCCT + GGGA			+			-+-			+				+			-+-				42999

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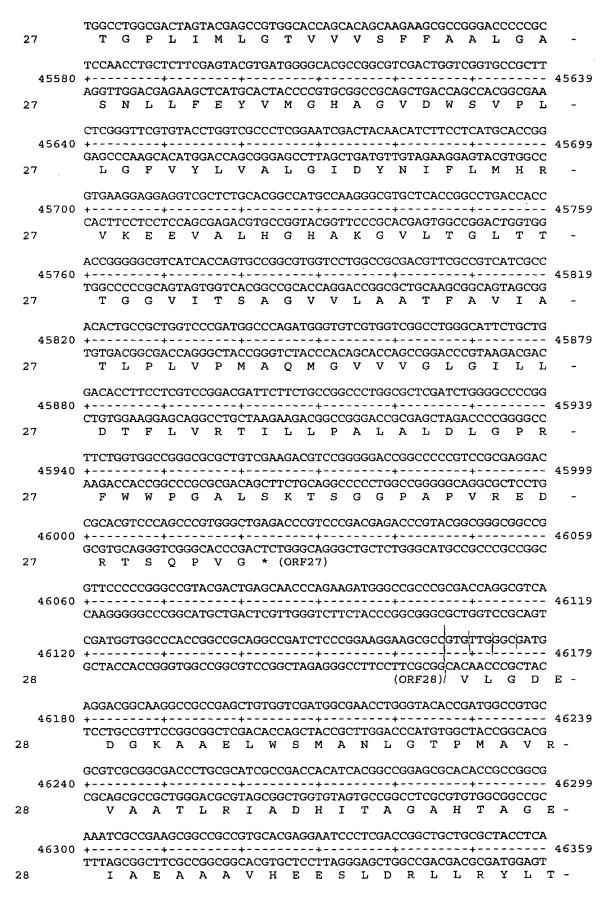


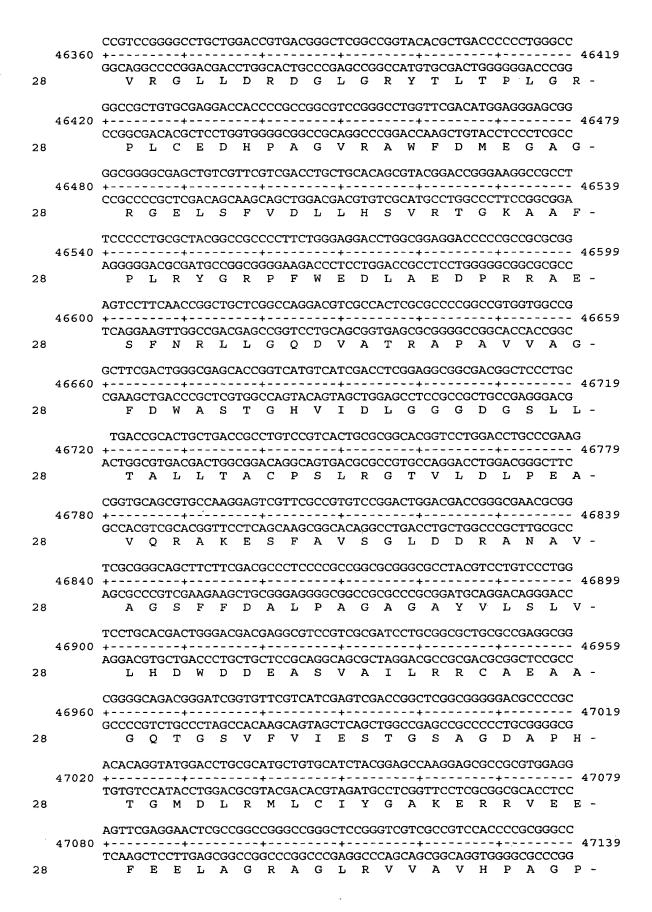


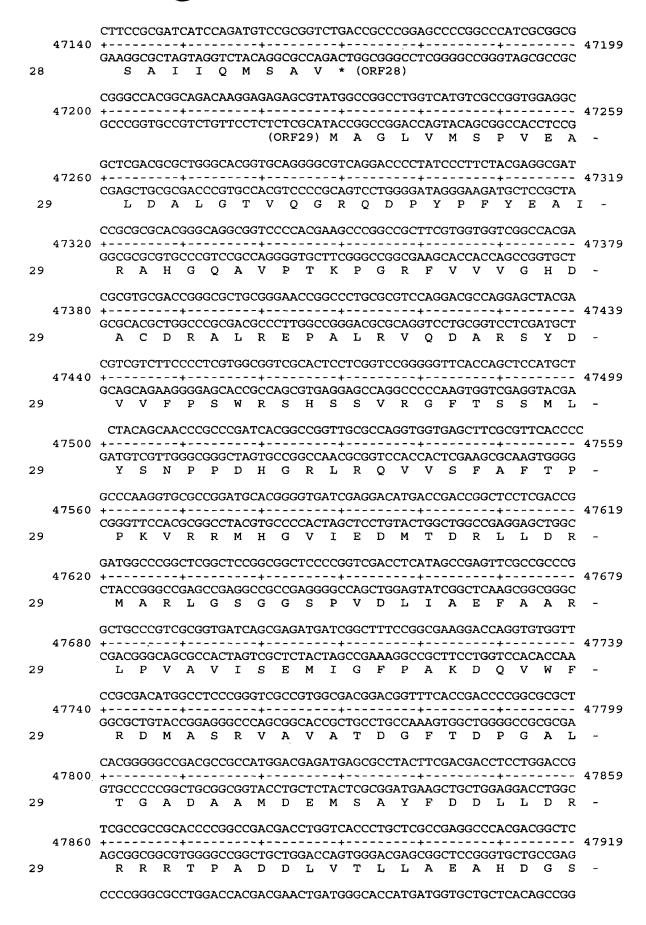


44740								,												44799
27																			CGGAC C L	
21	K	3	G	P	A	1	ינ	A	3	A	G	1	τ.	A	_	G	L	V	СЪ	-
	GTCC'	TCG	CGG.	ACG	TCA	ACT	CCT	CCC	GCT	CCA	TGC	GCC	TGG	TCG	GCG	CGA	TCG	GCG'	TGGTC	
44800																				44859
27																			ACCAG V V	
21	V	ш	A	ט	V	1/4	5	3	Д	5	141	G	ъ	V	G	A	_	G	v v	-
	TGCG	CCC'	TCC'	TCG	CCA'	TGG'	TCA	CGA'	TCC	TGC	CCC	CGC	TGC	TGG	TCA	TCC	TGG	GCC	GCTGG	
44860																				44919
0.7																			CGACC R W	
27	C	A	ப	ш	A	Ivi	٧	1	7	ш	P	A	ъ	יי	V	_	ш	G	K W	-
	GTGT'	TCT	GGC	CCT	TCG'	TTC	CCC	GCT	GGA	CGC	CGC	AGI	CGG	CCG	CGG	CCC	C.CG.	AGG	CACCG	
44920																				44979
27																			GTGGC A P	
21	V	r	W	P	F	v	P	K	W	1	P	E.	3	А	A	A	P	-	A P	-
	GCGT	CCC	ACA	GCC	GCT	GGG	AGC	GCA'	rcg	GCT	CCG	TCF	CGG	CCG	CCC	GGC	CGC	GCC	GCGCC	
44980																				45039
27																			CGCGG R A	
21	Α.	Q	11	3	К	**	12	K	1	G	J	٧	1	Α.	Α	K	F	K	K A	_
																			ACATG	
45040																				45099
27																			TGTAC D M	
21	**	٧		5		Ω	^	-	G		_	^		5	5	ы	9		D 14	
																			AGCGG	
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27																			TCGCC E R	
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																			GCGCG	
45160																				45219
27																			CGCGC S A	
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																			AGGAC	
45220																			TCCTG	45279
27						-		_		_	-		-						Q D	
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45000																			TTCCC	
45280																			AAGGG	45339
27																			V P	_
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27								_											L V	
45400																			GGGTC	45459
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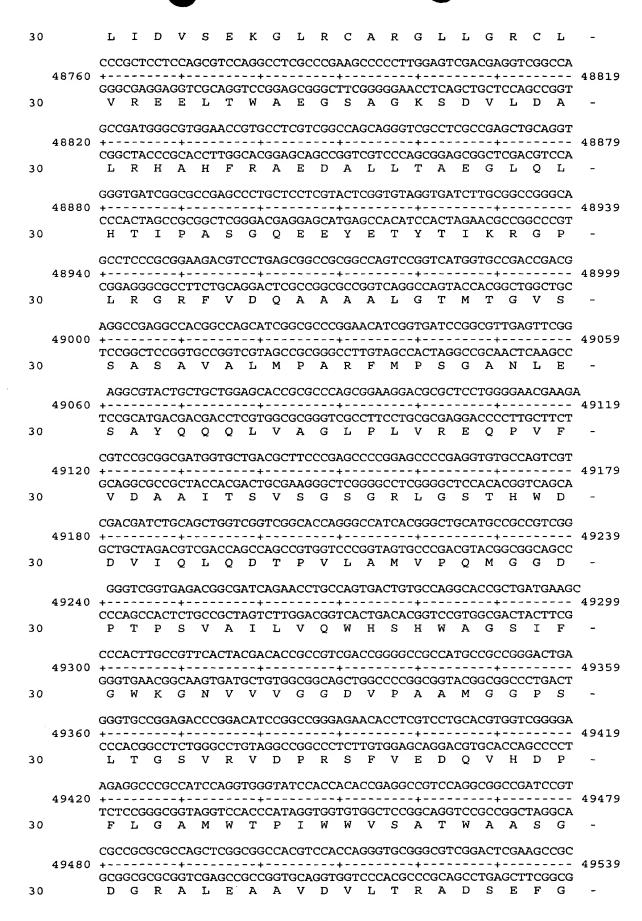


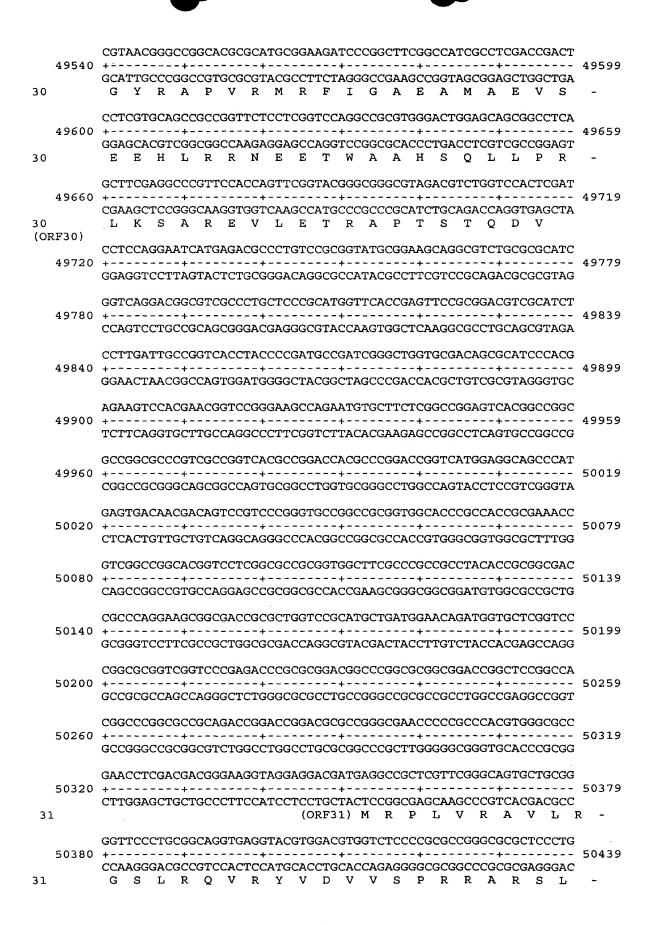
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29	47920	GGGGCCCGCGGACCTGGTGCTTGACTACCCGTGGTACTACCACGACGAGTGTCGGCC  P G R L D H D E L M G T M M V L L T A G	17979 -
	47980	GTTCGAGACCACGAGCTTTCTGATCGGCCACGGGGCGATGATCGCCCTCGAACAACGGGC	18039
29		CAAGCTCTGGTGCTCGAAAGACTAGCCGGTGCCCCGCTACTAGCGGGAGCTTGTTGCCCG F E T T S F L I G H G A M I A L E Q R A	-
	48040	GCACGCGGCCCGGCTGCGGGCCGAACCCGACTTCGCCGACGGCTACGTCGAGGAGATCCT	18099
29		CGTGCGCCGGGCCGACGCCCGGCTTGGGCTGAAGCGGCTGCCGATGCAGCTCCTCTAGGA H A A R L R A E P D F A D G Y V E E I L	-
	48100	CAGGTTCGAGCCGCCGGTCCACCAGCCGGTGGGCTGCCGAGGACCTCGACCTGCT	8159
29		GTCCAAGCTCGGCGGCCAGGTGCAGTGGTCGGCCACCCGACGGCTCCTGGAGCTGGACGA R F E P P V H V T S R W A A E D L D L L	-
	48160	GGGCCTGTCCGTACCGGCGGGCTCCAAGCTGGTCCTGATCCTGGCCGCCGCGAATCGCGA	18219
29		CCCGGACAGGCATGGCCGCCGAGGTTCGACCAGGACTAGGACCGGCGCGCGTTAGCGCT G L S V P A G S K L V L I L A A A N R D	-
	48220	TCCCGGCCGCTACCCCGAGCCCGGCCGGCCGGCCGGCCGG	18279
29		AGGGCCGGCGATGGGGCTCGGGCCGAAGCTGGGGCTGGCGATGCGCGGGCCC PGRYPEPGRFDPDRYAPRG	_
	48280	CGGGCCGGAGGCCACCAGACCGCTGAGCTTCGGCGCGGGCGG	18339
29		GCCCGGCCTCCGGTGTCTGGCGACTCGAAGCCGCGCCGC	-
	48340	TCCGCTGGCGCGGCTGGAAGCCCGGATCGCGCTGCCGCGTCTGCTGCGCCGCTTCCCGGA	18399
29		AGGCGACCGCGCCGACCTTCGGGCCTAGCGCGACGCGCGAGGGCCTPLAREAR LEARIALPRLLRFPD	-
	48400	CCTGGCCGTGTCCGAGCCCCCGTCTACCGCGACCGCTGGGTCGTCCGCGGCCTCGAAAC	18459
29		$\begin{array}{cccccccccccccccccccccccccccccccccccc$	-
	48460	CTTTCCCGTGACCCTCGGGTCCTGAGCCCCCGCCGGCCGG	18519
29		GAAAGGGCACTGGGAGCCCAGGACTCGGGGGGCCGGCCTTGTGCACTGGCAGGGCCGG F P V T L G S * (ORF29)	
	48520	GGCGGGTGCGCCCTCTCAGACGTACAGGGTGTTGGGCCCCTGACCACACACA	18579
		CCGCCCACGCGCGGGAGAGTCTGCATGTCCCACAACCCGGGGACTGGTGTCTCGTGGGCC	
	48580	CCGTACAGCTCCAGGTTGGTGCTCGGGTTCATGCAGGTGCAGCGTGATGCTCTGGGCATC  +	18639
3 (	)	(ORF30)* A P A A H H E P C	
	48640	GCTGCACGCGCTGGATCGGGACGTCGTTGTAGATCGAGGACCCGCCGCCGCCTCGCCTGGGCGA	18699
30		CGACGTGCGCGACCTAGCCCTGCAGCAACATCTAGCTCCTGGGCGGCGAGCGGACCCGCT R Q V R Q I P V D N Y I S S G G S A Q A	-
	48700	GGATGTCCACCGACTCCTTGCCCAGTCGGCACGCCCCCAGCAGGCCGCGCACAGCA	18759





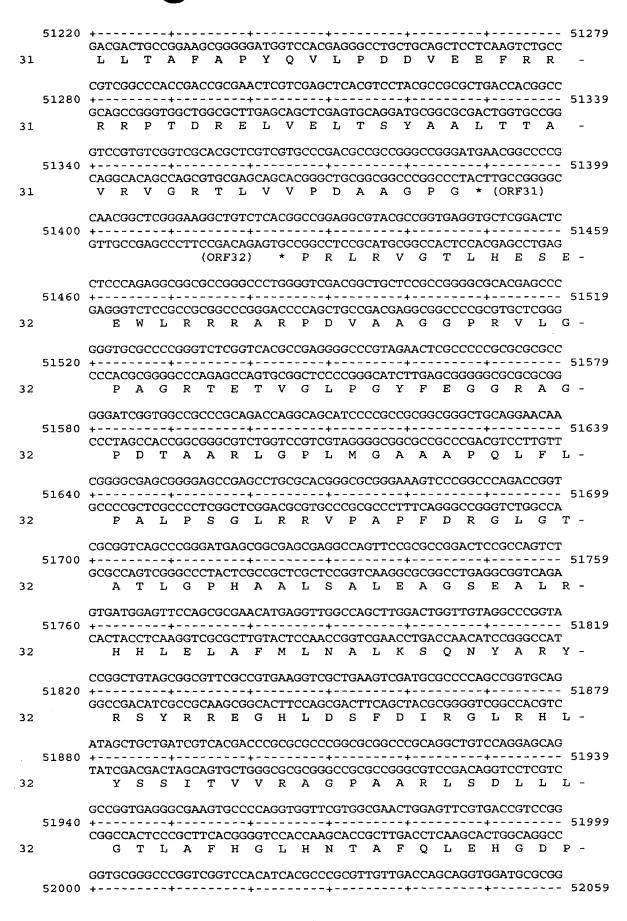




	50440	+	10499
	30440	CACCGCGCCCACATGGCCCTCTGGCTCCAAGCCGCACGAGCGCGGGGGGGACCGG	,0133
31		V A R V Y R E T E E Q F G V L A P P L A	-
		CTCCACTCGCCCGCGCGCGTCGCTGGCCGCGACGTGGCTCATGCTGCGGGAGACACTG	
	50500	+	0559
		GAGGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	
31		LHSPAASLAATWLMLRETL	-
		CTGGTCGACGGGCGGTGAGCCGGGCGGTGAAGGAGACGGTCGCCACCGAGGTCTCCCGT	
	50560		0619
31		GACCAGCTGCCCGCCCACTCGCCACTTCCTCTGCCAGCGGTGGCTCCAGAGGGCA L V D G R V S R A V K E T V A T E V S R	_
	50620	GCCAACGACTGTCCGTACTGCGTCCAGGTCCATCAGGCGGTACTCGGGACACTGCCTCCG	0679
	30020	CGGTTGCTGACAGGCATGACGCAGGTCCAGGTAGTCCGCCATGAGCCCTGTGACGGAGGC	,0075
31		ANDCPYCVQVHQAVLGTLPP	-
		GACGGCGGCCAGGCCGGGCTCCTGCGGTGGGTCCGGGAGGCAGGC	
	50680	+5	0739
2.1		CTGCCGCCGGTCCGGCCCGAGGACGCCACCCAGGCCCTCCGTCCG	
31		D G G Q A G L L R W V R E A G R R P G G	
		GGTGCGGTGGGCGGCGGCCGCTTCCGTTCAGCGGTGAACAGGCACCGGAACTGTGC	
	50740	+5 CCACGCCACCCGCCGCCGCCGCGAAGGCAAGTCGCCACTTGTCCGTGGCCTTGACACG	0799
31		G A V G G G R P L P F S G E Q A P E L C	-
	50800	GGCGTCGTGGTCACGTTCCACTACATCAACCGCATGGTCTCCCTCTTCCTCGACGACTCC	0859
		CCGCAGCACCAGTGCAAGGTGATGTAGTTGGCGTACCAGAGGGAGAAGGAGCTGCTGAGG	
31		GVVVTFHYINRMVSLFLDDS	-
		CCCATGCCGACCCCGACGCCGACACCGTTGCGCGGGCCCATCATGAGGACCACCGCACTG	
	50860	+	0919
31		GGGTACGGCTGCGGCTGTGGCAACGCGCCCGGGTAGTACTCCTGGTGGCGTGAC PMPTRTPTPLRGPIMRTTAL	_
31			
	50000	GCCATGCGTCCGGCCCGGGGCTGCTGACACCGGGCGCATCGCTCGGCCTGCTGCCT	
	50920	+5 CGGTACGCAGGCCAGGCCCCGACGACTGTGGCCCGCGTAGCGAGCCGGACGACGAC	10979
31		AMRPVGPGLLTPGASLGLLP	-
		CCGGCTCCCCTGCCGCCCGGACTGGAGTGGGCCGAGGGCAACCCTTTCGTGGCCCAGGCG	
	50980	+5	1039
		GGCCGAGGGGACGGCCTGACCTCACCCGGCTCCCGTTGGGAAAGCACCGGGTCCGC	
31		PAPLPPGLEWAEGNPFVAQA	-
		CTGGGGCGTGCCGTCGCCGCTGTGGACCAGGGAGCGCACTGGGTGCCCGAACCGGTCCGG	
	51040	45	1099
31		GACCCCGCACGGCACACCTGGTCCCTCGCGTGACCCACGGGCTTGGCCAGGCC  L G R A V A A V D Q G A H W V P E P V R	_
	51100	GAGCGGCTGCGCACACGTCTGGACACCTGGGACGGATCGGCCGGGCCTCGGCCGGGGA	1150
	31100	CTCGCCGACGCGTGTGCAGACCTGTGGACCCTGCCTAGCCGCGGCCCGGAGCCGGCCCCT	,1135
31		E R L R T R L D T W D G S A P G L G R G	-
		TGGCTCGACGAGGCCGTGTCCGGCCTGCCGCCCCAGGACGTGCCCGCGGCACGGCTGGCG	
	51160	+5	1219
31		ACCGAGCTGCTCCGGCACAGGCCGGACGGCGGGGGTCCTGCACGGGCGCCGTGCCGACCGC W L D E A V S G L P P Q D V P A A R L A	_
ЭT		"	
		CTGCTGACGGCCTTCGCCCCCTACCAGGTGCTCCCGGACGACGTCGAGGAGTTCAGACGG	

 $\tt GTGGCGCGGGTGTACCGGGAGACCGAGGAGCAGTTCGGCGTGCTCGCGCCCCCCTGGCC$ 

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32		CCACGC	CCGGG R A			GGTG'		GCG( V			ACAA N			L L			ACG(		P -
	52060	GAAGCG																	52119
32	32000	CTTCGC		CGTC	CAAG		CGCG		GTG	CGT	GC?	rgce	CTC	CTGC	CCC	TTT	CTAC	GTC	
	52120	CCGTCT + GGCAGA	+ CTGGC	AGTO	CAAC	+- GCGG	 CTGC	CGT	- + - · GGG(	CCG	AAA	+- CCTA	CGC	CCC	GCC	+ 3GCC	 3CCC	CTG	
32			R V			~						~							J -
32	52180	CCCGCG + GGGCGC G	+ CAGGC	CTAG	CGC	+-	 CGGT	 CGT(	- + - 3GT(	GCA	 CCC	+ - GCGG	CAC	CGGC	CCC	+ 3CTC	CGAC	GAC	
		CGCCAG																•	~
32	52240	+ GCGGTC A	CACGT	CAGG	CTA		CTCG	ACC	GTG(	GCC2	ACTO	GTC	GCC	GCCA	ACC!	AAGO		ATGC	
32		GTCCGG + CAGGCC	+	GCCG	 CCG	+- CGAG	 GTCG	CAG	- + - · CGG(	GGC#	AAGA	+ - AGTA	GCC		CAGO	+ GGAC			52359
	52360	GATGCG + CTACGC	TCAGC	CGGC	CTG	GGCCI	ATCG	CGG	CCC(	3GT <i>I</i>	AGC(	CGTT	GGC	GAC	GA:	rct(	- <b>-</b>	- <b>-</b> -	52419
	52420	GGAGTG + CCTCAC	+	- <b>-</b> -		+-		<b></b> - ·	-+-	- <b>-</b> -		+-	·			+	- <b>-</b> -	- <b></b>	52479
	52480	GTTGAA + CAACTT	+			+-			-+-			+-				<b></b>			52539
	52540	TCCCTC + AGGGAG	+			+-			-+-	<b>-</b>		+-				+ ~			52599
	52600	CTCGGC + GAGCCG	+			+-			- <b>+ -</b> ·	- <b>-</b> -		+ -				+	- <b>-</b> -		52659
	52660	GGCGAG + CCGCTC	+			+-			-+-		- <b></b> -	+ -				+			52719
	52720	GTGGGA + CACCCT	+			+-			-+-			+-				+			52779
	52780	GCGTTG + CGCAAC	+			+-			-+-	<b>-</b>		+-	- <b>-</b> -			+			52839
	52840	CGGTGC + GCCACG	+			+-			-+-			+-			- <b>-</b> -	+			52899
	52900	GAGTGC																	52959

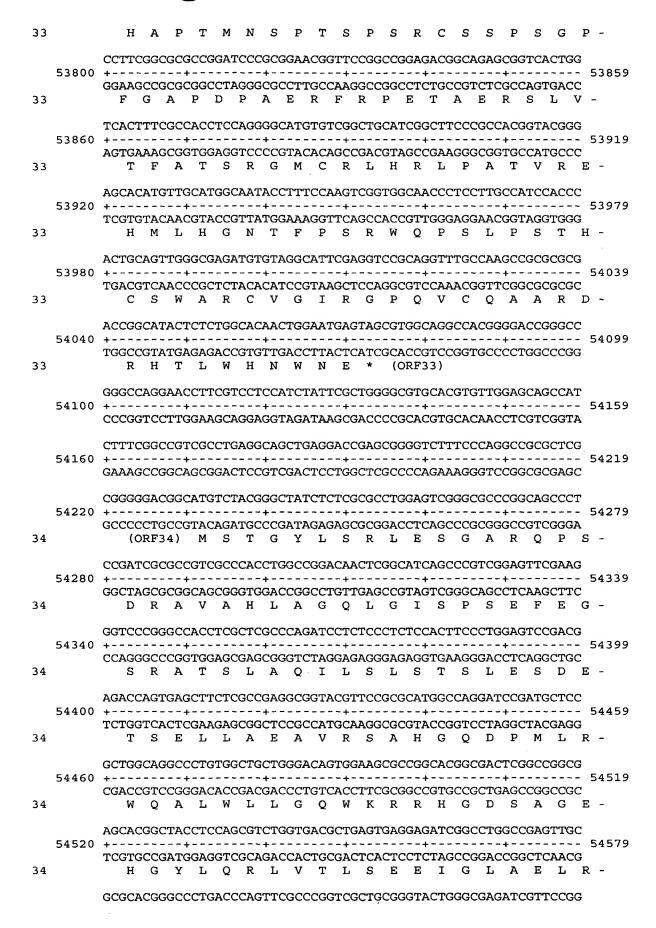


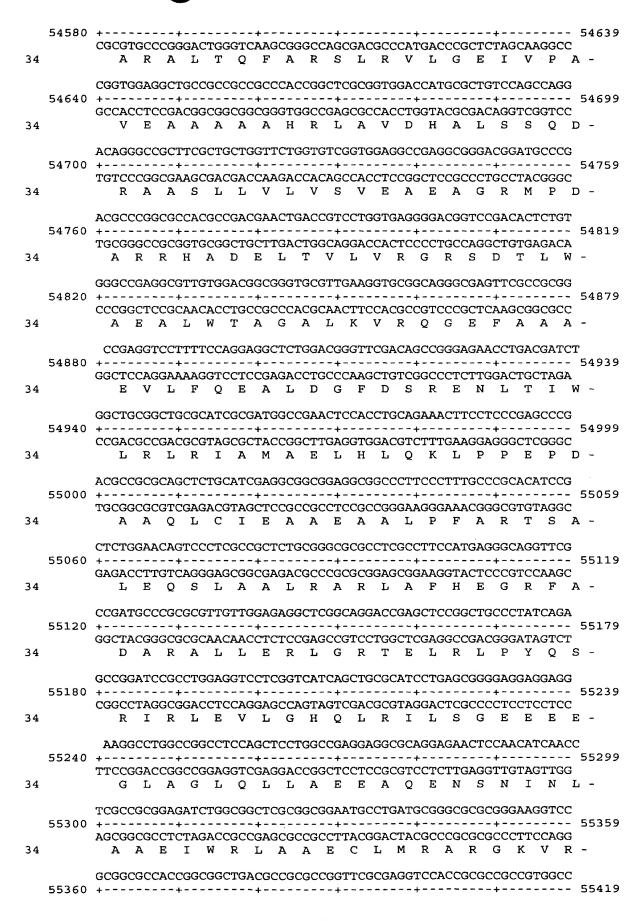


		CTCACGATACACCCCGTGCCGAGAAGGCCCCACCTGCTCCCCGCCTGCCGCCTA	
	52960	CAGGGCCATTCGACTTCGTCGTCGGCGGCCGCGCAGATGCGGGTGAAGGGCCATTCCACG	.9
	32,00	GTCCCGGTAAGCTGAAGCAGCCGCCGCCGCGCGCGCTCTACGCCCACTTCCCGGTAAGGTGC	
	53020	TCTTCCCCTCCCGTTGCGGAGTGGGCGGAGGCCGTGGTGAAGAGGGTGACGAGTCCGAAC +	19
	53080	GTGCCGAAGAGGGACAGTCGGGCAACGTGAAGTGCGGTACCCATGCGAGCTCCTAGC +	39
	53140	GAGGGCGGCGTGACCGCGGGACGTGAGACCTCGTGATGCCAGGAAGCTAGCGAATCGGA +	9
33	53200	CTGAGGGTGGCAACGATATGCCAGACTTTGGCAACTTGCCTGTGTATCAGCCGGACTGTC +	59
33	53260	GGCCGCTGGTAAAGACGGAACGGCGAGATCCCGCGACCGCGTCGCAGAGCAGCAGGGTCT +	19
33	53320	GCTCACCCAGCGTCGGGGCGGCCAGCATGTCGCGTACCGGGAGCGTGACGCCCAGCTCGC +	79
33	53380	GGTTGATCCTGCGGACCAGCCGGGTGATGAGCAGGGAGTCGCCGCCGTGGGCGAAGAAAT  +	39
33	53440	CAGCACCTTCGGAGGGGTCCGGGAAGCCGAGCAGGTCACCCCAGCCGCGCACCAGTACCT +	99
33	53500	GGCGGATGTCGCCGGTGACGACCGTGCGCCGGGAGCCCCGACGTGCCGAGCCCCGACGCCCCGACGCGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCAGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCGACGCCCCCGACGCCCCGACGCCCCGACGCCCCCGACGCCCCGCCCCCGACGCCCCGCCCCCGACGCCCCCACGCCCCCGCCCCCC	59
33	53560	GCGAGGCATGCACCAGCGCCACCTGGTCGCCGAGGTTGCGCCGCGACAGCTCGCGCAGCG ) +	19
33		ACACCGTGACGCCGAACCTCTCGGTGATCCTGCGGACCAGCCGCGTGATCAGCAGCGTGT  ) +	79
33	53680	CCCCGCCGCGCGAGAAATCCGAATGCTCGGTGAGGTCGGAGCGCCGAGGAGCTCGC ) +	'39
	53740	TCCACGCGCCGACCATGAACTCCCCCACGTCACCGAGCCGGTGCTCGCCGTCGCGGGGC	199





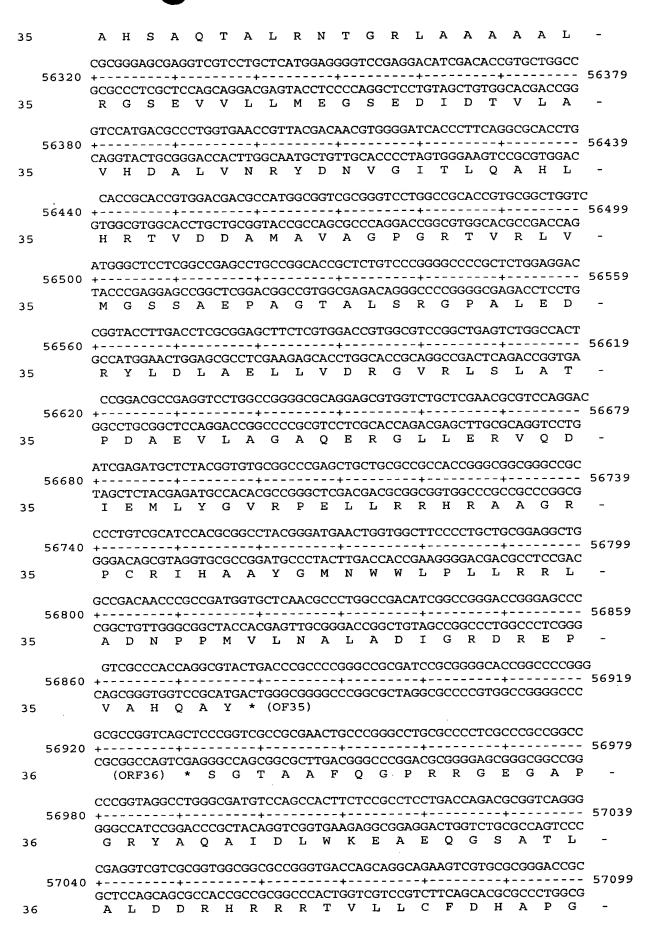




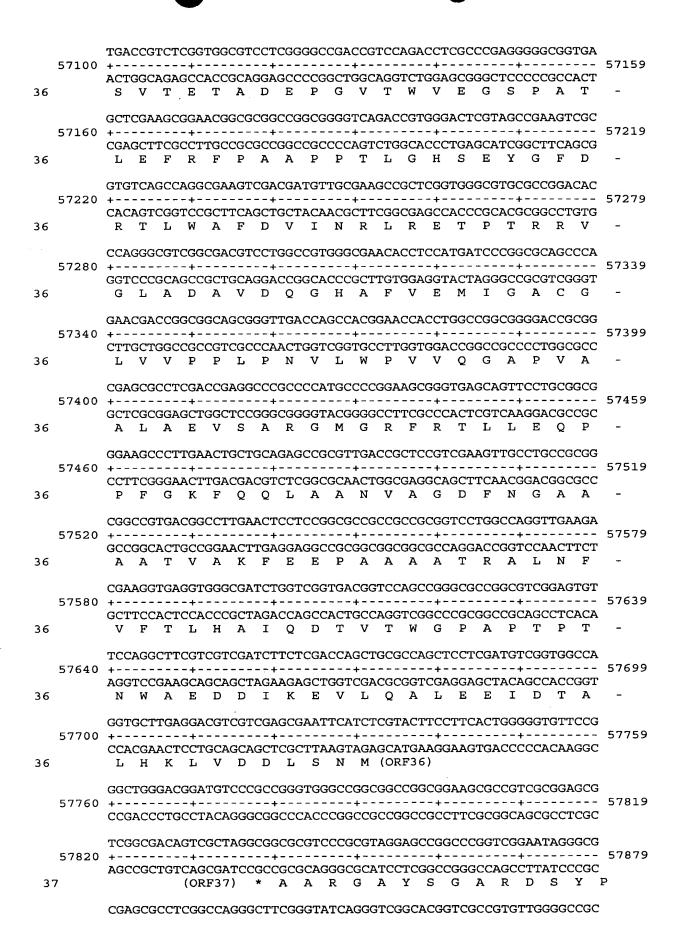




34		G A T G G * (ORF34)	
	55420	ACCGCCGTCGGCGTGAGGCGCCGCGTGTGCCCCCCCACGGTTGCTCGCCCTTGGTGG	55479
		TGGCGGCAGCCGCACTCCGCGGCCGCACACGGGGGGGTGCCAACGAGCGGGAACCACC	
	55480	TGCATCTGTTGGCACATGTGTACCTCCTACACAGTCAATTGTTGCCAAAATTGTCGAACC	55539
		${\tt ACGTAGACAACCGTGTACACATGGAGGATGTGTCAGTTAACAACGGTTTTAACAGCTTGG}$	
	55540	GAATGGCAATTGCTTGCCTGAAGAGGCGTGCTGATATGCAAGTCAAGTAGCCTCC +	55599
	55600	TCCGATCTCGGGCGGCCATATGGGAAACATCGAGTTGAGCGGCGATGGCGTTCGTCAGTG ++	55659
		CTGCCGTTCTGGCCAGGCAACTGATGTCGATGGGGATGGCAAGATTTTGCCGAAAACCGA	
	55660	#	55719
	55720	TACATCTCTGTCCGGACAGCCTTCGCCCCCGGGTGACACTGCTCCGGCATGGCT	55779
	•	ATGTAGAGACAGGCCGGCCTGTCGGAAGCGGGGGCCCACTGTGACGAGGCCGTACCGA	
	55780	CCGGTTTCTCGTCGCCCGGCCGACGGACCGCACCGTCCGGAACGAGCGCGCGGTGTGCGT ++	55839
	55840	CCGCTGATGGGCACAGCGGCCTCGGCCGCAGCAGGTTCCCACCGAGAAGAATGCCGAGGC	55899
		GGCGACTACCCGTGTCGCCGGAGCCGGCGTCGTCCAAGGGTGGCTCTTCTTACGGCTCCG	
	55900	CCAGCCGTGAACCACGACATGTCCCAGCGTGCCTTGCTGGAGGCGGCGGCCGAGGGGCTG +	55959
	55960	CGGCGGCTGGCCGCGCGCGCGCGCGCGCGCCTCCTCGGCATTG ++ GCCGCCGACCGGCCGCCGCCGCCGCCGCGCGCGGGAGGAG	56019
35	56020	AGGGACATGTTCTCCCCCGCCGCCGCCGGTACGTGCTCGCCTCGGACCGCGCGGGGTTC  ++ TCCCTGTACAAGAGGGGGCGGCGGGGCGCCCCAAG (ORF35) M F S P A A R R Y V L A S D R A G F	56079
		TTCGAGCAGGCTGTCCGGCTGCGCTCCCGGGGGTACCGGGTGAGCGCGGAGTTCGTCGGC	
35	56080	AAGCTCGTCCGACAGGCCGACGCGAGGGCCCCCATGGCCCACTCGCGCCTCAAGCAGCCG F E Q A V R L R S R G Y R V S A E F V G	56139
	56140	CCCGATCAGGGAGCCACCGACGCCCTCCACGCGGAGCACGTGGTCGAAGAGCACCTGAGG +	56199
35		PDQGATDALHAEHVVEEHLR	-
35	56200	CTGCTCGATCAGGAGCCGGCCCCTGACCGGATCGGTGTGGACGTCTCCCGGATCGGCCTC  ++ GACGAGCTAGTCCTCGGCCGGGGACTGGCCTAGCCACACCTGCAGAGGGCCTAGCCGGAG  L L D Q E P A P D R I G V D V S R I G L	56259 -
		GCCACTCGGCGCAGACTGCCCTGCGCAACACCGGGCGGCTGCCGCTGCGCGCGC	
	56260	+++	56319











37	57880	+	939
37	57940	GCATGCAGGCGATGCGCTGGCGTCCCCGCGCCACCAGGGTCTCGCCGCCGTCGTCGCCCA +	999
37	58000	GCTTGATGTAGTCGAAGGTGAACTCCAGCTGGGTCTGCCGCAGCTCCGAGAGCCTCATCC +	059
37	58060	GGATCGACAGTTCGTCGAAGGCGGTGATCTCCGCGAAGAACTCGCAGTCCACCTTGAGGG +	119
37	58120	TGAAGAGCTTGAGGTCCTCCTGGACCTCGGCGAGCACCGAAGGCGCCCTCTCCTTGAGAA +	179
37	58180	AGAGTTCCCGGCAACGCCCCTGCCAACGAAGGTAGTTGACGTAGAAGACGTTGCCGACGA +	3239
37	58240	GGTTCGTCTCCTCGAAGCCGACGGTGTGGCGGAGCTCGAAGTAGTCAGGATTCGTCGCGG +	3299
37	58300	TCATAGGTCTGTGCCCTTCGTCGGGGCCGGTCGTCGCACCGAGTTGCGTGAAGCAAC +	3359
	58360	TCACTGGTCGCGATGGCCTGCGGGGTCGGTGGCCCGCGCTCCGGGCGGAGAGTGCGGGCG +	3419
38		GGGTGCCGGCCGGGGGTCAGCCGCGCGCGCGCACAGGGGAAGAACCCTCTCG +	
38	58480	CGGCCGCTCGTGGAGCCGTCGGGGGCCGGTGCGCCGTAGGTGACGGAGATACCCCGGCTC  +	
38		TGCGCGGCGCACGATCCCCGGCATCGCGCGTTCGGCGAGCGCCGCGATGGTCATCGCG  +	
38		GGATTGACCGTCAGCGCCGGGAACCGACGATCCGTCGGTGACGAAGATCCCCGGGTGG  +	
	58660	TCGCGGAGCTCGTTGCTGTCGTCCAGGGCGGATGTGTGGGGGGTCGTCGCCCATCCGGCAG  +	8719



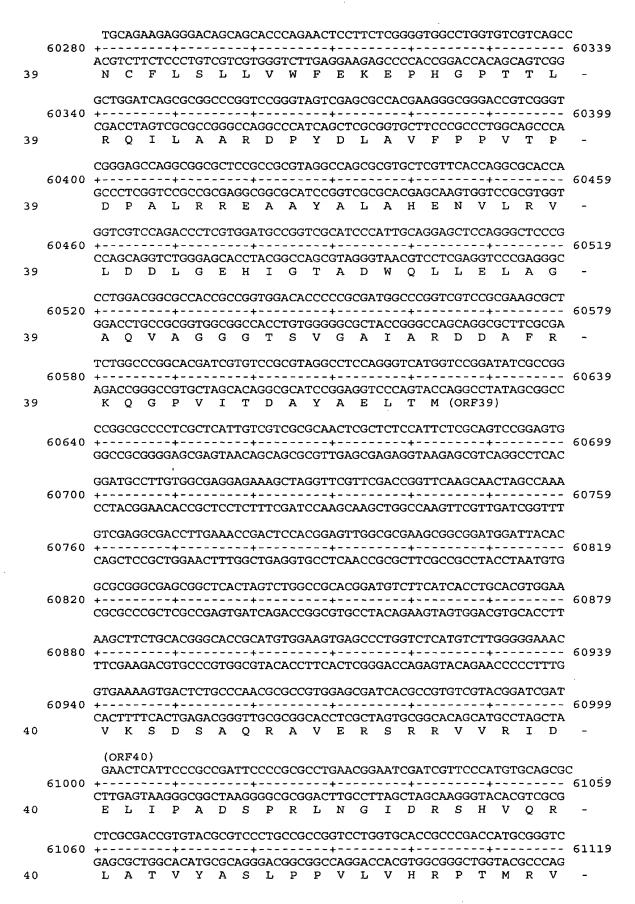


38		D	R	L	E	N	s	D	D	L	Α	s	T	Н	P	D	D	G	M	R	С	_
	58720	GAGGA +		<b></b> -	+			- +			+				+	<b>-</b>		- +				58779
38			S	L	P	Н	V	Т	Y	Α	G	V	L	D	N	Т	W	P	M	V	K	-
38	58780	+	 CCG(	GCA	+ GGA		GGT(	- + - · CCT2	AGA(	 3GA/	+ ACT(	GGA	 GCC	GCA	+ : GCC:	rac(		- + - 3GG'	 rcc	GCGC	G G	58839
2.0	58840	TCCC		AGA	+ : AGC		CCA	-+- GCA:	rcg	 CGT(	+ CCA	ACG	 GGG	CCG	+ · GCT(	CGT	AGA	- + - CGA		TCT?		58899
38	58900	CGGT	GGG	CGT'	TAC	CGG:	rgg	CGG	GAG	GGG	GGC:	CGA.	AGA	CGC	CTT	CGT:	rgt(	CGT	CCT	CGA:	гC	58959
38	30700	GCCA	CCC	GCA	ATG	GCC G	ACC	GCC	CTC	CCC	CCG	GCT'	TCT	GCG	GAA(	GCA.	ACA	GCA D	GGA D	GCT/ E	AG I	-
38	58960	ATCG + TAGC M	<b>-</b> ACT'		+ AGC	ACT	cgg'	-+-	rcc	AGG	+ rga	 CGA	 AGT	CCT.	+	GGA	AGA	- + - AGA	 GGA		GC	59019
38	59020	TTGG		TCC	+	GGC	ACC	- + - GCG	GCC		+ GGA	ccc	 GCT	CCT	+ AGC			-+-	<b></b> -		cc	59079
38	59080	TTCA	 TCT	 CGA	+ CAA		 CCC'	- + - TCA	 TCG	 CCC'	+ TCA	TGA	GCC	<b>-</b> CGT	+ <b>-</b> - TGC'	 TCG		-+-		- <b></b>		5 <b>91</b> 39 -
38	59140	CAGC + GTCG W	 AGC	 GGT	+ GCC		 CGG	-+- GGA	 ACG	 GCT.	+ AGA	 CCA	ACC	 GGC	+ GCA	TCC	 GCT	-+- CGG	GCA		GG	59199
30	59200	CGGT + GCCA	CCA  GGT	GGC 	CGA + GCT	ACA  TGT	GCT  CGA	CGG -+- GCC	CCG  GGC	CCT  GGA	TGG + ACC	CCT  GGA	CGT  GCA	CGA  GCT	TGA + ACT	TGG  ACC	CGG  GCC	TGT -+- ACA	TGA  ACT	 'C <b>G</b> G	 CG	
38	59260	TCGC	CGT	TGC	CGG +	AGA	AGT	AGC	GTC	CGA	CCG	CTC	GTG	GCA	.TGG +	TGC	CCA	.GGT -+-	GGG		CG 	59319
38		E CTGC	G GCT	N GGA	G .GGA	S .TCA	F .CCG	Y GGG	R TCG	G CGC	V CCG	A CGC	R CGG	P CCG	M CCA	T TCA	G .CCA	L .CGA	H TCT	A TCG	E	<del></del>
38		+ GACG	 CGA	 CCT	+ CCT	 'AGT	 GGC	-+-	AGC	 GCG	+ GGC	GCG	GCC	 GGC:	+ GGT:	AGT	 GGT	-+- GCT'	 'AGA		GG	59379
38		AGCT E	ACT I	GCG V	+ GCG G	ACG S	GGC G	-+- GGA A	CCT Q	CCG	+ CCA R	TCA Y	AGC#	GCA D	GCA D	.CGT H	GCI V	GCA V	ACA N	TCA Y	.CG H	59439
38		TGGG		TCC	+ TCG	GCA	GCC	- + -	'ACG	CGC	+ TCT:	CCF	ACG <i>I</i>	 \CCT	+ GGA	GCA	CGT	-+-	CCC		'AC	59499

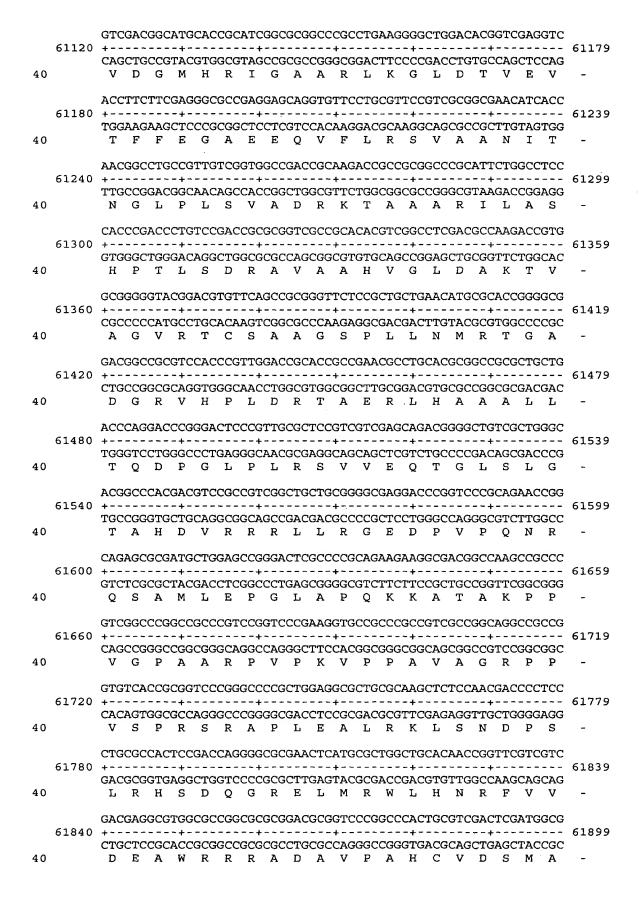




		CGCGCCCCATGGGCGATGGCGGCGGGCAGGTAGTTGACCAGCAAGGACTGCTTGGCCTCG	
	59500	GCGCGGGGTACCCGCCGCCCCCTCCATCAACTGGTCGTTCCTGACGAACCGGAGC	9559
38		RAGHAIAAPLYNVLLSQKAE	-
		AAGCGGCAGCCGGCCATCATCCAGTTGCAGTTCACGCACTTGGTGTTGTCGATGGCGACG	
	59560	TTCGCCGTCGGCCGGTAGTAGGTCAACGTCAAGTGCGTGAACCACAACAGCTACCGCTGC	9619
38		F R C G A M M W N C N V C K T N D I A V	-
		GCGAGGGGTTGGCGGTGCGCCGGCGTGGTTGCACGCCGGCCCCACAGTCCGCCGGCG	
	59620	+5	9679
38		CGCTCCCCAACCGCCACGCCGGCCCCACCAACGTGCGCGCGGGTGTCAGGCGGCCGC A L P N A T R G A H N C A A A W L G G A	_
		The Cotton agreements and anagement account an agent amount of a company of	
	59680	TAGCTCACGTCGTTCCAGTCCTGCCGGGTCACGGAGAGGGACTCCTCGACACGGTCGTAC	9739
38		ATCGAGTGCAGCAGGTCAGGACGCCCAGTGCCTCCCCTGAGGAGCTGTGCCAGCATG Y S V D N W D Q R T V S L S E E V R D Y	
30			_
	59740	CAGGGGTCCAGGGTTTCGCGGCTCACCGCCTGCGGCCACATCCGGCGTCCTATGGACCCC	9799
	33,10	GTCCCCAGGTCCCAAAGCGCCGAGTGGCGGACGCCGGTGTAGGCCGCAGGATACCTGGGG	,,,,
38		WPDLTERSVAQPWMRRGISG	-
		TGCCGGTCGAAGACGAAGCGCGGGGCGCGGGGCATCGCGGCGAAGTAGACGACGCTGCCG	
	59800	ACGGCCAGCTTCTGCTTCGCGCCCCGCGCCCCGTAGCGCCCCCTTCATCTGCTGCGACGGC	9859
38		Q R D F V F R P A R P M A A F Y V V S G	-
		CCGCCCACACAGTTCCCGCCGAGGATGCTCATGCCGTCCCCGACCGTGAAGTCGAACGCC	
	59860	+5 GGCGGGTGTCAAGGGCGGCTCCTACGAGTACGGCAGGGGCTGCACTTCAGCTTGCGG	9919
38		G G V C N G G L I S M G D G V T F D F A	-
		CTCGTGTACGAGGAGCCGAGTTTGTAGTCGTGCTCGAACTCCTTGCTCTCCAGCCACGGC	
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38		$egin{array}{llllllllllllllllllllllllllllllllllll$	-
		CCGCGTTCCAGGACGTGACGTCGGCGCCCCCCCGCCAGGTGGTAGGCGGCGATGGCA	
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38		GGCGCAAGGTCCTGCCACTGCAGCCGCGGGGGGGGGGGG	_
		CCGCCGAATCCGCTGCCGATGACGAGGACGTCCGTGCGCTCGGCCGTGGTGCTCATGCGG	
	60040	+6	0099
38		GGCGGCTTAGGCGACGCTACTGCTCCTGCAGGCACGAGCCGGCACCACGAGTACGCC G G F G S G I V L V D T R E A T T S M	
30		(ORF39) * A	- ,
		GGCTCCCGGTGGACGTGTCGGGGTGGAGGCGGGCGAACTCACGCCCGTAGCTGTAAT	
	60100	+6	0159
39		CCGAGGGCCACCTGCACCACCTCCGCCCGCTTGAGTGCGGGCATCGACATTA PSGTSTTDPHLRAFERGYSY	-
		CCTTGAAGCGCCACAGGCCGTCGGCGTCCGGCATGCTCAGGCCCATGGCCTCCAGTCCCG	
	60160	+6	0219
39		GGAACTTCGCGGTGTCCGGCAGCCGCAGGCCGTACGAGTCCGGGGTACCGGAGGTCAGGGC D K F R W L G D A D P M S L G M A E L G	_
	60220	GATGGCCGTCCTCCATCGCCTGTGCCGTGTTGAGGTGCGCGGCCGAATCGAAGGCCATGT +	0279
2.0		CTACCGGCAGGAGGTAGCGGACACGGCACAACTCCACGCGCCGGCTTAGCTTCCGGTACA	
39		PHGDEMAQATNLHAASDFAM	-











40	61900	GAGCTGGCGCACCACTGCTCGGACGCCTGGCACCGGTTCGCCGAGGAGATGGTTCGGCGC ++ CTCGACCGCGTCGTGACGAGCCTGCGGACCGTGGCCAAGCGGCTCCTCTACCAAGCCGCG E L A Q H C S D A W H R F A E E M V R R	61959 ~
40	61960	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	62019
4]		$\begin{array}{cccccccccccccccccccccccccccccccccccc$	62079
41		GGTCGTCGAGTACATGCACGTCAACCTGGGTCAGAACCTCACGATCGAT	
41	62140	CACGGCGATGTTCAGCAAGTTCCATTTCACCCGCATCTTCCGCGAAGTCACCGGTACCTC ++ GTGCCGCTACAAGTCGTTCAAGGTAAAGTGGGCGTAGAAGGCGCTTCAGTGGCCATGGAG T A M F S K F H F T R I F R E V T G T S	62199 -
41	62200	TCCCGGGCGTTTCCTGTCCGCCTTACGGATTCAGGAGGCCAAGAGACTTCTCGTGCACAC  + AGGGCCCGCAAAGGACAGGCGGAATGCCTAAGTCCTCCGGTTCTCTGAAGAGCACGTGTG P G R F L S A L R I Q E A K R L L V H T	62259
41	62260	TGCACTCAGTGTGGCCGATATCAGCAGTCAGGTCGGCTACAGCAGTGTCGGTACTTTCAG ++ ACGTGAGTCACACCGGCTATAGTCGTCAGTCCAGCCGATGTCGTCACAGCCATGAAAGTC A L S V A D I S S Q V G Y S S V G T F S	62319
41	62320	TTCTCGCTTCAAGGCCTGTGTGGGGCTTTCCCCGAGCGCCTATCGCGACTTCGGCGGGGT ++ AAGAGCGAAGTTCCGGACACACCCCGAAAGGGGCTCGCGGATAGCGCTGAAGCCGCCCCA S R F K A C V G L S P S A Y R D F G G V	62379 -
41	62380	GCAGCCGGGTTTTCCCTCCGCCGCGGCCCGTCTCACTCCCACCGCGCACAATCCCTCCGT ++ CGTCGGCCCAAAAGGGAGGCGCGCGCGCGCAGAGTGAGGGTGGCGCGTGTTAGGGAGGCA Q P G F P S A A A R L T P T A H N P S V	62439 -
41	62440	GCGCGGCCGCATTCACTCCGCCCCGGGTGACAGGCCCGGAAGGATCTTCGTGGGCCTGTT ++ CGCGCCGGCGTAAGTGAGGCGGGGCCCACTGTCCGGGCCTTCCTAGAAGCACCCGGACAA R G R I H S A P G D R P G R I F V G L F	
41	62500	CCCCGGCAGGATGCGCCAGGGCCGCCCGGCGCGCGCGCGC	
41	62560	CTTCGAGCTCCGGGACGTGCCCGTGGGCACCTGGCACATCCTGGTCCACTCCTTCCCCGC ++ GAAGCTCGAGGCCCTGCACGGGCACCCGTGGACCGTGTAGGACCAGGTGAGGAAGGGGCG F E L R D V P V G T W H I L V H S F P A	62619 -
41	62620	CGGACACCGGCCGCACCAGCTCGACTCCGAACCGCTGTTGCTCGGGCACAGCGGACCGCT ++ GCCTGTGGCCGGCGTGGTCGAGCTGAGGCTTGGCGACAACGAGCCCGTGTCGCCTGGCGA	62679





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	62740	CCTCGAT																	62799
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42		s v	T M	P	L	G	G F	R M	R	L	S	L	M	P	E	A	V	A	-
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	62920	+	+			-+-			+			+	- - -		-+-			·	62979
42	62920	-	+ AGTA	GGGC'	TCCA	· - + - \ACG	ACGO		+ : CGTC:	 rtgg		+	GGC		-+- GCT	TGC	CCT	AC	
42	62920	CGGAGGT A E	+ AGTA M	GGGC' M G	TCCA L	AACG N	ACGO S	GCTG(GTC: CGTC:	rtgg F	 CCC R	+ CGG P	G G	GCG A	-+- GCT G	TGC F	CCT P	CAC I	
42		CGGAGGT	AGTA M ACCG	GGGC' M G	TCCA L CGGT	ACG N	ACGC S	G V	CGGG	TTGG F GGTT	CCC R	P	GGCT	GCG A	-+- GCT G	TGC F	CCT P	TAC I CGC	-
		CGGAGGT A E TACGCGT	AGTA M ACCG + TGGC	GGGC M G CGGC GCCG	TCCA L CGGT	AACG N CCGG	ACGC	GCTG(G V CTG(AGAC(CGTCT CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTGG F GTT	CCC R CGA	P ACC	GGCT GGCT GCGA	GCG	GCT G G GGT -+-	TGC F CGA	P AGC	CAC I CGC	- 63039
42		CGGAGGT A E TACGCGT	AGTA M ACCG + TGGC	GGGC M G CGGC GCCG	TCCA L CGGT	AACG N CCGG	ACGC	G V	CGTCT CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTGG F GTT	CCC R CGA	P ACC	GGCT GGCT GCGA	GCG	GCT G G GGT -+-	TGC F CGA	P AGC	CAC I CGC	- 63039
	62980	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT	AGTA M ACCG+ TGGC Y CCTC	GGGC GGGC GCCG R P	TCCA L CGGT GCCA R	ACCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACGO S CGGT GCCA A	GCTGC G V CTGC AGACC T (CGTCT CCGGG CCGGC R	TTGG F GGTT CCAA P	CGA CGA GCT E	PACC	GGCT GGCT GCGA R	GCC CGG CGC CGCC	GGT GGGT CCA P	TGC F CGA CCT D	AGC	CAC I CGC GCG R	- 63039 -
	62980	CGGAGGT A E TACGCGT + ATGCGCA Y A	ACCG ACCG TGGC Y CCTC	GGGC' M G CGGC' GCCG R P	TCCA L CGGT GCCA R	ACGG NCGGG AGCC DCCCG	ACGC S CGGT GCCA A	GCTG(CTG(CTG(CTG(CTG(CTG(CTG(CTG(CTG(CTG	CGTCTCCGGGCCGGCCC	TTGG F GGTT CCAA P	CCCA R CCGA CCT GCT	ACC F	GGCT GCT GCGA R	GCG A CGGG GCC E	GGT GGGT -+- CCA P	TGC F CGA .GCT D	AGC TCG F	CGC I CGC R	- 63039 -
	62980	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT	ACCG ACCG TGGC Y CCTC GGAG	GGGC' M G CGGC' GCCG R P	TCCA L CGGT GCCA R AGCC	AACG N CCGG AGCC D CCCG	ACGC S CGGT GCCA A GATC	GCTG(G \ TCTG(T () GGCG(CCGC(CGGCCGGCCCGGCCCGGCCCGGCCCCGGCCCCGGCCCCCGGCCCC	TTGG F GGTT CCAA P ATGA	CCC R CCGA CCT E TGT	ACC F TGG F	GGCT GCT GCGA R GGGC	GCG A CGG GCC E	GGT GGGT CCA P	TGC F CGA .GCT D	AGC TCG F	CGC I CGC R	- 63039 -
42	62980	CGGAGGT A E TACGCGT ATGCGCA Y A TCGGGGT AGCCCCA	ACCG ACCG Y CCTC GGAG D	GGGC' M G CGGCG GCCGG R P CCAC GGTG GGTG	CGGT CGGT GCCA R AGCC	ACG N CCGG C-+- AGCC D CCCG CCCG	ACGO S CGGT GCCA A GATO CTAO	GCTG(G V TCTG(AGAC(T (GGCG(H I	CCGGGGCCGGCQ R CTGCCCGGGCCQ R CTGCCCGGCCQ R CTGCCCGGCCQ R	TTGG F GGTT CCAA P ATGA ATGA TACT	GCT E TGT TGT	ACC F TACC Y	GGCT FCGA R GGCC CCCG	GCG A CGG GCC E AGA TCT	GGT GCCA PCCA CCA CCA CCA	TGC F CGA GCT D GCA	PAGC FACAT	CGC R CCC R CCC D	- 63039 -
42	62980 63040	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT + AGCCCCA E P	ACCG ACCTC Y CCTC GGAG D CGGA	GGGC' M G CGGCG R P CCAC GGTG' E W	TCCA CGGT GCCA R AGCC TCGG L	ACGGC D CCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGG	ACGC S CGGT A GATC CTAC P	GCTGG G \ TCTGG T () GGCGG T () GGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGCCCCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TTGG F GGTT CCAA P ATGA TACT M	CCCC R CCGA CCGA E TGT ACA I	ACC F ACC F ACC Y	GGG R GCGA R GCGA P	GCCA	GGT CCA P CCA CCA P CCA CCA CCA CCA CCA CCA	CGA CCGA CCGA CCGA CCGA	PAGCOTTCO F CAT	CGC R CCC AGG D	- 63039 - 63099 -
42	62980 63040	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT + AGCCCCA E P	ACCG ACCTC Y CCTC GGAG D CGGA GCCT	GGGC' M G CGGCG R P CCAC GGTG' E W CACC	TCGA R AGCO L CTGT	ACGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACGC S CGGT A GATC CTAC P CGCC	GCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGCC CCGGCC PGCCC R STGCZ CACGC R H CACGC	TTGG F GGTT CCAA P ATGA TACT M	CCCC R CCGA CCGA E TGT TACA I	PACCO	GGG R GCGA R GCGA P	GCCA	GGT CCA P CCA CCA P CCA CCA CCA CCA CCA CCA	TGC F CGA GCT D CGCT L TGG TGG TGG TGG	AGC F CGTA V GGCA	CGC R CCC AGG D	- 63039 - 63099 -
42	62980 63040	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT + AGCCCCA E P GATCCGG + CTAGGCC S G	ACCG ACCTC Y CCTC GGAG D CGGA GCCT	GGGC' M G CGGCG R P CCAC GGTG' E W CACC	TCGA R AGCO L CTGT	ACGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACGC S CGGT A GATC CTAC P CGCC	GCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGCC CCGGCC PGCCC R STGCZ CACGC R H CACGC	TTGG F GGTT CCAA P ATGA TACT M	CCCC R CCGA CCGA E TGT TACA I	PACCO	GGCT GGCT FCGA R GGCC P	GCGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	-+- GGT GGGT -+- CCA P CCA CCA CCA CCA CCCA CCCA CCCA C	TGC F CGA GCT D CGCT L TGG TGG TGG TGG	AGC F CGTA V GGCA	CGC R CCC D	- 63039 - 63099 -
42	62980 63040 63100	CGGAGGT A E TACGCGT + ATGCGCA Y A TCGGGGT + AGCCCCA E P GATCCGG CTAGGCC	ACCG ACCTC Y CCTC GGAG D CGGA+ GCCT A	GGGC' M G CGGCGR P CCACC GGTGG E W CACCC GTGGG S V	TCGA R AGCO L CGGT CGG	ACGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACGC S CGGT A GATC CTAC P CGCC	GCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGCC CCGGCC PGCCC R STGCZ CACGC R H CACGC	TTGG F GGTT CCAA P ATGA TACT M	CCCC R CCGA CCGA E TGT TACA I	PACCO	GGCT GGCT FCGA R GGCC P	GCGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	-+- GGT GGGT -+- CCA P CCA CCA CCA CCA CCCA CCCA CCCA C	TGC F CGA GCT D CGCT L TGG TGG TGG TGG	AGC F CGTA V GGCA	CGC R CCC D	- 63039 - 63099 -